

# STIC Search Report Biotech-Chem Library

#### STIC Database Tracking Number: 119347

TO: Minh-Tam Davis

Location: rem/3a24/3c18

Art Unit: 1642

Tuesday, April 13, 2004

Case Serial Number: 09/763335

From: Barb O'Bryen

**Location: Biotech-Chem Library** 

Remsen 1A69

Phone: 571-272-2518

barbara.obryen@uspto.gov

#### Search Notes

Tam,

Paul Schulwitz assisted me with the Score/Length search. There were no hits that met your criteria of length between 60-200 nucleotides, and score over length value of 70% or greater. Consequently, there is no print-out for that segment of the search.

Please let me know if you have questions.

Barb



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Minimum
Maximum
                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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DB seq length: 2000000000
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1: geneseqn1980s:*
2: geneseqn1990s:*
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geneseqn2003cs:*
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geneseqn2000s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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10886 498 10886 40862	16724 16724	2390 2390 333 429	671 261 716 716 1171	812 2058 1936	Length
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AAA44625 AAC94550 ABL34135 ABL34073	AAZ3334 AAC7939 ADA71938 ABL33091 ABL34537 ABL70260	ADB62738 AAC25659 AAX51967 AAH99019	AAK52784 AAC08673 AAL58347 ADB48315 AAI60133	AAK51800	ID
AAA44625 HUMAN SEC AAC94550 Cat flea Abl34135 Human imm Abl34073 Human imm	33334 Human se 79939 Human se 71938 Rice gen 33091 Human im 34537 Human me 70260 Chemical	8 Human 9 Human 7 Human 9 Human	Human Human Human Novel	Aaz51528 Human cel Abq77548 Human pho Abx71301 Human kid Aaks1800 Human pol	Description

mat\_peptide

/\*tag= 460. .7 /product= 385. .459

\*tag= . 783

'product= "Mature cell-signalling protein-2"

Location/Qualifiers

80

\*tag=

"Cell-signalling protein-2"

sig\_peptide

WPI; 2000-246562/21

Tang YT,

Corley NC,

Patterson C,

Guegler KJ,

Baughn MR;

(INCY-) INCYTE PHARM INC.

21-AUG-1998; 21-AUG-1998;

98US-00137578. 98US-0150689P. 99WO-US019072

19-AUG-1999; 02-MAR-2000. WC200011169-A2

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### ALIGNMENTS

### fungal infection; cytostatic; antiarthritic; antiasthmatic; immunosuppressive; antiarteriosclerotic; anti-HIV; antidiabetic; antiinflammatory; neuroprotective; antipsoriatic; antimicrobial; Human cell-signalling protein-2; CSIG-2; BRAINOT12 cDNA library; neoplastic disorder; neurological disorder; immunological disorder; vesicle trafficking disorder; smooth muscle disorder; asthma; emphysema; rheumatoid arthritis; HIV; human immunodeficiency virus; osteoporosis; multiple sclerosis; artherosclerosis; diabetes mellitus; psoriasis; irritable bowel syndrome; viral infection; bacterial infection; Homo AAZ51528 standard; cDNA; 812 BP Human cell-signalling protein-2 cDNA. AAZ51528; sapiens. (first entry)

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New human cell signaling proteins and polynucleotides useful for diagnosis, prevention and treatment of neoplastic, neurological, immunological, vesicle trafficking and smooth muscle disorders.
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Query Match

Sequence

BP;

609 A; 402

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610 T; 0 ÐΒ

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Score 686;

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Length 2058; 0 Other;

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RESULT 2
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ID ABQ7
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                                        The invention relates to human phosphorylcholine/ethanolamine transferase 3.35 (AAM43386) and nucleic acids encoding it (ABQ77548). The protein has a molecular weight of 9.35 kD. The invention also relates to a method for the recombinant production of the protein, an antagonist of the protein, and the use of the protein, gene and antagonist in therapeutic applications. Phosphorylcholine/ethanolamine transferase 9.35 can be used in the treatment of a variety of diseases such as lung hypectasia, disorders of bile acid metabolism, angiocardiopathy, related tumours, immune disorders and inflammatory conditions. The present sequence represents cDNA encoding human phosphorylcholine/ethanolamine transferase
                                                                                                                                                                                                                                               New polypeptide-human phosphorylcholine/ethanolamine transferase 9.35 treating lung hypectasia, bile acid metabolic disturbance disease, angiocardiopathy, related tumor, inflammation and immunological disease
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P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes novel polymucleotides and polypeptides isolated from human cDNA libraries which can be used for gene therapy or in vaccines. The polymucleotides of the invention and antibodies encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The products of the invention may also be used to identify modulators of expression and activity and to down regulate expression and activity. The antibodies of the invention may also be used as diagnostic agents for detecting the presence of polypeptides in samples. This sequence encodes a polypeptide described in the disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; gene; gene therapy; vaccine; disease treatment; detection; ss
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28-SEP-1999;
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 ACTCCCTGACAATTCTGGATGGATGTGCGCAACAGGCAACAAAATTAAGACCACGAGAAT
                                                                ACTGATTGGGAAATGGTGGTGTGAGATGGAGCCTTGCCTAGAAGGAGAAGAATGTAAGAC
                                                                                                              TCTACCTGGAAAAGTGGCTGGAACAACAAGAAACCGGCCTTCTTGCGTCGATGCCTCCAT
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                                                AGTGATTTGGAAATGGTGGTGAGATGGAGCCTTGCCTAGAAGGAGAAGAATGTAAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                             53.3%; Score 433.2; DB 5; ilarity 96.1%; Pred. No. 1e-117; Conservative 0; Mismatches 18;
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               Query Match 53.
Best Local Similarity 99.
Matches 432; Conservative
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27-APR-2000;
20-JUN-2000;
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                                                                                                                                      The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activiny inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system diagraes, archittis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the common of the contraction of cancer activity are missions.
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15-SEP-2000;
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, Zhao QA,
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2000US-00560875.
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27-APR-2000; 2000US-00598075.

20-JUN-2000; 2000US-00598075.

19-JUL-2000; 2000US-00620325.

01-SEP-2000; 2000US-00654936.

15-SEP-2000; 2000US-00663561.

20-OCT-2000; 2000US-0069325.

20-OCT-2000; 2000US-00728422.
                                          Tang
Ma Y,
e AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human
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WPI; 2001-476283/51.
P-PSDB; AAM79651.
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                                                    g YT, Liu C,
Y, Zhao QA,
AJ, Yang Y,
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Wejhrman
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J, Zhang J,
Goodrich R;
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J, Ren
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Wang
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RESULT 6
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DT 06-C
DT XX
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      encoded polypeptides (AAM/80302) And State with it activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The prolypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hammonomodulatory activity and activity tissue growth factor activity, immunomodulatory activity and activity in the diagnosis and/or treatment of cancer, leukaemia, nervous system discorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581) 2111 (AAK52582) and 3666 (AAM(80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding polypeptides with cytokine-like activities, in diagnosis and gene therapy.
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                                                                                                                    06-OCT-2000
                                                                                                                                                                                   AAC08673 standard; cDNA;
                                gene therapy;
                                                 Human; 5' EST;
                                                                                Human secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention relates to polynucleotides (AAK51456-AAK53435) and the
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                                                                                                                    (first entry
                                ; expressed sequence tag; secreted chromosome mapping; ss.
                                                                              protein 5'
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98.6%;
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Pred. No. 1.3e-115;
); Mismatches 6;
                                                                                     SEQ ID NO: 12748
                                                     protein; cDNA isolation;
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sapiens

Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;

Human polynucleotide SEQ ID

NO 550

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XGXGXGXGXGXGSSSSSSSSSSSXX
RESULT 7
AAI58347
IID AAI58
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AAI68
AC AAI5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 12748; 71pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid that is a 5' expressed sequence tag (5' EST) obtaining cDNAs and genomic DNAs that correspond to 5'ESTs an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dumas Milne Edwards
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 261 BP; 70 A; 72 C;
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                                                                                                                  22-OCT-2001
                                                                                                                                                                                AAI58347 standard; cDNA;
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                                                                                                                                                                                                                                                                                                 TGAATGAAC 189
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                                                                                                                  (first entry)
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98.9%;
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Pred. No. 4.7e-45;
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Wang
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                                                                                                                                                                                                                                                                                                                                    immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous
                                                                                                                                                                                                                                                                                                                                                                              The invention
                                                                                                                                                                                                                                                                                                                                                                                                                     Novel nucleic acids and polypeptides, useful as central nervous system injuries.
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                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                           and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form
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                          GAAAAGTGGCTGGAACAACAAGAAACCGGCCTTCTTGCGTCGATGCCTCCATAGTGATTG
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                                                 GGCAGGTGGCAGGCACCACGCGAGCTGCTCCATCATGTGTGGATGCTTCAATAGTGGAAC
                                                                                         GCTGTAATAAGAACAAGATAGAAGAACGGTCACAAACAGTCAAGTGCTCCTGCTTCCCTG
          <u>AGAAATGGTGGTGCCATATGCAGCCATGTCTAGAGGGAGAAGAATGTAAAGTTCTTCCGG</u>
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GAAAAGTGGCTGGAACAACAAGAAACCGGCCTTCTTGCGTCGATGCCTCCATAGTGATTG
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The invention relates to a polynucleotide comprising a sequence given the specification, or its mature protein-coding portion, or its complement. The polynucleotide is useful for treating diseases e.g., cancer or neurodegenerative diseases and many others listed in the specification. The present sequence represents a novel human cDNA. Not The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPT approach to the control of the printed specification but was obtained in electronic format directly from USPT approach to the control of the control of the printed approach to the control of the control
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GCTGTAATAAGAACAAGATAGAAGAACGGTCACAAACAGTCAAGTGCTCCTGCTTCCCTG
                                             GTTGTAACAAGAATCGCATTGAGGAGCGGTCACAAACAGTAAAGTGTTTCCTGTCTACCTG
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                                                                                                                                                                                                                                                                                                                                     Wang
Zhou
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immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathes and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
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                                                                                                                               The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic,
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DB; AAM40977.
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Wang Z, Wek
Goodrich R,
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2000US-00552317.
2000US-00598042.
2000US-00620312.
2000US-00653450.
2000US-00652191.
2000US-00693036.
2000US-00693036.
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Wehrman T,
                                                                                                                                                                                                                         system
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                                                                                                                                                                                                                                                                                                                                   nrman T, Xu C,
Drmanac RT;
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Yang
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Zhang J,
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Zhao QA;
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Best Local Sim
Matches 202;
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                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human;
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     Isogai
                                                                                              05-NOV-2001;
25-JAN-2002;
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     Sugiyama
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                                                                                              2001JP-00379298.
2002US-00350978.
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                                        INST.
BIOTECHNOLOGY.
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     H
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       Otsuki
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       Wakamatsu
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Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and c.N.S disorders. Note: The sequence data for this patent did not form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1171 BP; 329 A; 265 C; 321 G; 254 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  479 AGCAGCATCACCTGCACAGACCAGAAGGAGGGACGTGTGAAGTGATAGCAGCACCACCGAT
                                                                                                                                                                                                                                                      ss; gene; pharmaceutical; diagnostic; gene therapy; regeneration; cell regeneration; membrane protein; transcription-related
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                                                                                                                                                                                                                       uction-related protein; transcription-related neurological disease; cancer; tumour.
/product= "Clone NT2NE20069580 protein"
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Pred. No. 3.5e-28;
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Sato

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The invention discloses a polynucleotide comprising a sequence selected cc from 1970 fully defined nucleotide sequences which encode novel cc polypeptides. Also claimed is a polypeptide encoded by the polynucleotide or its partial peptide, an antibody binding to the polypeptide or peptide cc of the polynucleotide, immunologically assaying the polypeptide or peptide cc with the antibody of the encoded protein, and observing the binding cc with the antibody of the encoded protein, and observing the binding cc between the two, a transformant carrying the polynucleotide in an cc expressible manner and an antisense polynucleotide. The oligonucleotide is useful as a primer for synthesising the polynucleotide, or as a probe cf useful as a primer for synthesising the polynucleotide, or as a probe cf detecting the polynucleotide. The polynucleotide and encoded genes may be included in them, for developing a diagnostic marker or cc medicines for regulation of their expression and activity, or as targets of gene therapy. The genes are involved in tissue and/or cell cranscription-related proteins, signal transduction-related proteins, represented is a collar to the activity or as targets encoding them can be used as indicators for diseases (e.g. osteoporosis, neurological diseases, cancer, tumours. The cDNA may be used to regulate the activity or expression of the encoded protein not treat diseases. The sequence presented is a cDNA of the invention. Note: Some of the sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the European Patent Office.
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Best Local
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  gene
                              Human; 5' EST;
                                                                                  Human secreted
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                                                                                                                                                                                                                                            AAC25659 standard;
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  therapy;
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Yoshikawa
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chromosome mapping; ss.
                                                                               protein
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Pred. No. 3.3e-27;
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M, Nagahari K, Masu
                                                                                     SEQ ID
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                              secreted protein; cDNA isolation;
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S B Ş B 5

06-SEP-2000

Homo sapiens

thrombolytic;

anti-inflammatory; tumour inhibition;

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RESULT 12
AAX51967
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Best Local S
Matches 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. ESTs are derived from mRNAs with intact 5' ends and can therefore be us to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.
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                                         Human; secreted protein; EST; expressed sequence tag; diagnosis; forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopolesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                           Human secreted protein 5'
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                                                                                                                                                                                                                                                                                                                                                       682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAGGAGGGACGTGTGAAGTGATAGCAGCACCACCGATGTTGTAACAAGAATCGCATTGAGG
                                                                                                                                                                                                                                                                                                                                                                                   GCTGCTCCATCATGTGGATGCTTCAATAGTGGAACAGAAATGGTGGTGCCATATGCAG
                                                                                                                                                                                                                                                                                                                                                                                                             ACCG-GCCTTCTTGCGTCGATGCCTCCATAGTGATTGGGAAATGGTGGTGGTGAGATGGAG 681
                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
                                                                                                                                                                                                                                                                                                                                                       AAACGGGAACTTGTGAGGTGGTGGCACTCCACAGATGCTGTAATAAGAACAAGATAGAAG
                                                                                                                                                                                                                                                                                                                       CCATGTCTAGAGGGAGAAGAATGTAAAGTTCTTCCGGATCGGAAAGGATGGA
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                                                                                                                                                                         (first
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                                                                                                                                                                                                                                          DNA;
                                                                                                                                                                           entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 109.6; DB pred. No. 4.2e-22
                                                                                                                                             SEQ ID NO: 181.
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RESULT 13
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AC AAH99
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Best Local S
Matches 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequences can be used for producing secreted human gene products. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell proliferation/differentiation activity, haematopoiesis regulating activity, tissue growth regulating activity, reproductive hormone regulating activity, chemotactic/ chemokinetic activity, haemostatic and thrombolytic activity, receptor/ ligand activity, anti-inflammatory activity tumour inhibition activity or other activities. The products can be used in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptide can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human secreted proteins, and encode the proteins given in AAY12987 to human secreted proteins. The proteins given represent the signal peptide AAY13219, respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid and an N-terminal fragment of a secreted human gene products. They
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            may have cytokine, immune, regulatory, haem, inflammatory or tumour inhibition activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                      Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; tomato; monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;
                                                                                                                                                                                                                                                                       AAH99019 standard; cDNA; 429
                                                                                                                                                                Human
                                                                                                                                                                                                 12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                      therapy; nutrition; ss
                                                                                                                                                                EST-derived
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                                                                                                                                                                                                                                                                                                                                                                                    TGCAATGCTACTCTGCCATGGATCCCTTCAGC 469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCAGAGAATGGCAATGGTCTCTGCGATGTCCTGGGTCCTGTATTTGTGGATAAGTGCTTG
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                                                                                                                                                            coding sequence SEQ ID NO:
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Pred. No. 7
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RESULT 14
AAZ33334
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17-JUL-2000;
03-AUG-2000;
15-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cow, pig, hamster, monkey, macaque, yeast, urchin and tomato. These were derived from from the organism of interest. They can be forensics, gene mapping, identification of biodiversity and for nutritional purposes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a cDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-JAN-2001; 2001WO-US002687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the invention
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                                                                                      Human, secreted protein; nutritional; cytokine; cell proliferation; differentiation; immune stimulating; vaccine, suppression; haematopolesis regulation; tissue growth; activin; inhibin; chemota chemokinetic; haemostatic; thrombolytic; receptor; ligand; anti-inflammatory; cadherin; tumour invasion suppressor;
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                                                                            inhibition; gene therapy; ss.
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; 2000US-00617746.
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; 2000US-00663870.
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                                                                                                                                                                                               (first entry)
                                                                                                                                                                   protein clone ml243_1 nucleotide sequence SEQ
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A, Zhang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65.2%;
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Pred. No. 3
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                                                                                                                        chemotactic;
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                                                                                                                                                                          ID NO:37
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RESULT 15
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22-JUL-1998;
31-JUL-1998;
31-JUL-1998;
10-AUG-1998;
11-AUG-1998;
06-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        treating, preventing or ameliorating medical conditions in humans and animals. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity, haematopoiesis regulating activity, tissue growth activity, activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, anti-inflammatory activity. The polymucleotides are also stated to be useful for gene therapy. AAZ33316 to AAZ33373 encode human secreted proteins, and AAY52998 to AAY53060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      isolated from adult placenta, adult retina, foetal brain, foetal kidney adult blood, adult brain, adult thyroid, adult bladder, adult neural tissue, adult testes, and adult lymph node cDNA libraries. The human secreted proteins, and the polymicleotides encoding them, are predicted to have biological activities which would make them suitable for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotides encoding secreted human proteins, placenta, adult retina, fetal brain, fetal.
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                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1493 BP;
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AAC79939 standard;
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DB; AAY53016.
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                                                                               CTGGAGGGGGAAGGCTGCGACTTGTTAATCAACCGGTCAGGCTGGACGTGCAC
                                                                                                              CCCGCCTGTGTGGACGCAAGAATCATCAAGACCAAGCAGTGGTGTGACATGCTTCCGTGT
                                                                                                                                                                              CCTTCTTGCGTCGATGCCTCCATAGTGATTGGGAAAATGGTGGTGAGATGGAGCCTTGC
                                                                                                                                                                                                             CGGCAGACCGCCCGCTGTGCGTAGAAAGGGGCAGATCGCCGGCACCACGAGAGCCCGG
                                                                                                                                                                                                                                                                              invention describes new human secreted proteins which were
                                                                                                                                                                                                                                                                                                                                              Conservative
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Pred. No. 0.00011;
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Steininger RJ,
                                                                                                                                                                                                                                                                                                                                                                                                              T; 0
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Sequence 2469

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Contractivitic, antirheumatic, antiproliferative, cytostatic, cardiant, controle, cerebroprotective, nootropic, neuroprotective, antiproliferative, cytostatic, cardiant, convircide, fungicide and ophthalmological activity and which can be used convircide, fungicide and ophthalmological activity and which can be used convircide, fungicide and ophthalmological activity and which can be used convircide, respectively, and (II) are used to prevent, treat or ameliorate a condition in e.g. humans, mice, rabbits, goats, horses, cats, condition or susceptibility to a pathological condition. The control of the discrete and in diagnostic immunoassays e.g. radioimmunoassays corexyme linked immunosorbent assays (ELISA). Disorders which are condition discreted arthitits, hyperproliferative disorders e.g. rheumatoid fungions or treated include autoimmune diseases e.g. rheumatoid control of the prevent disorders e.g. cardiac arrest, cerebrovascular conditions, cardiovascular disorders e.g. cardiac arrest, cerebrovascular conditions of the condition or superior conditions caused by bacteria, viruses and condition, for supporting cell culture of primary tissues, to condition, for supporting cell culture of primary tissues, to conditiate mammalian metabolism, to change mammalia state or compitive qualities, as a food additive or preservative, such as to conjutive qualities, as a food additive or preservative, such as to conjutive qualities, vitamins, minerals, cofactors or other nutritional
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated human secretory proteins, nucleic acids encoding them and antibodies directed against them, useful for diagnosing and treating disorders related to the proteins such as cancer, Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-MAR-2000; 2000WO-US006042
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03-DEC-1999;
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Pred. No. is the number of results predicted by chance to have a

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SUMMARIES

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TITLE	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AY325120	RESULT 1
Rupp, F. TAFA: A Novel Secreted Family with Homology to CC-chemokines	Tang, Y.T., Emtage, P., Funk, W., Hu, T., Arterburn, M., Park, E. and	1 (bases 1 to 801)	Mammalia; Eutheria; Rodentia; Sciuroqnathi; Muridae; Murinae; Mus.	Mus musculus	Mus musculus (house mouse)		AY325120.1 GI:32967238	AY325120	Mus musculus TAFA1 mRNA, complete cds.	AY325120 801 bp mRNA linear ROD 23-JUL-2003		

ALIGNMENTS

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2 (bases 1 to 801)
Tang, Y.T., Emtage, P.,
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Location/Qualifiers
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                                                                                            AGAACCTAACAGAAGCATTTGTGGTAGTAAAGGAA 812
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                                                                                                                              GACAATTCTGGATGGATGTGCTACAGGCAACAAGATTAAGACTACACGAATTCACCCA
                                                                                                                                                     GACAATTCTGGATGGATGTGCGCAACAGGCAACAAAATTAAGACCACGAGAATTCACCCA
                                                                                                                                                                                GGGAAATGGTGGTGAGATGGAGCCCTGCCTAGAAGGAAGAATGTAAGACACTCCCT
                                                                                                                                                                                                                                                                                   TGTTGTAACAAGAACCGCATCGAGGAGCGGTCACAAACAGTGAAGTGTTCCTGTTTACCT
                                                                            AGAACCTAACAGAAGCATTTGTTATATAAATAGGA
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(protein id="AAF92412.1"
/db xref="GI:32967239"
/db xref="GI:32967239"
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EVIAAHRCCNKNRIEERSQTVKCSCLEGKVAGTTRNRPSCVDASIVIGKWWCEMEPCL
EGEECKTLPDNSGWMCATGNKIKTTRIHPRT"
 301 from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
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Patent WO0112659.
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Pred. No. 8.5e-109;
0; Mismatches 78;
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              DNA
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AL713702
AL713702.1 GI:1958
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AX086349.1
                                               Bloecker, H.,
                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1936)
                                                                                                   Homo sapiens
             Direct Submission
Submitted (12-MAR-2002)
                                     Wiemann, S
  Martinsried, GERMANY
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/mol_type="unassigned DN/
/db_xref="taxon:9606"
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                                                  Boecher, M.,
                                                                                                                  (human)
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96.1%;
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              MIPS,
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DKFZp566B064 (from
                                                   Brandt, P.,
               Am
             Klopferspitz 18a,
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Mewes, H.W.,

Gassenhuber, J. and

linear PRI 20-MAR-2002 clone DKFZp566B064).

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Wiemann,S.
Wiemann,S.
Human dna sequences
Patent: WO 0112659-A 301 22-FEB-2001;
German Human Genome Project (DE)
German Human Genome Project (DE)
Tocation/Qualifiers
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TCACCCAAGAACCTAACAGAAGCATTTGTGGTAGTAAAGGAA
                              TCACCCAAGAACCTAACAGAAGCATTTGTGGTAGTAAAGGAA
                                                                                             ACTCCCTGACAATTCTGGATGGATGTGCGCAACAGGCAACAAAATTAAGACCACGAGAAT
                                                                                                                                ACTCCCTGACAATTCTGGATGGATGTGCGCAACAAGGCAACAAAATTAAGACCACGAGAAT
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Pred. No. 2.9e-104;
D; Mismatches 18;
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PRI 23-JUL-2003

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by GBF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 German Genome Project
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/translation="MAMVSAMSWVLYLWISACAMLLCHGSLQHTFQQHHLHRPEGGTC
EVIAAHRCCNKNRIEERSQTVKCSCLPGKVAGTTRNRPSCVDASIVIWKWWCEMEPCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue type="kidney"
/clone Tib="566 (synonym: hfkd2). Vector
Xl-2blue; sites NotI + SalI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type= ".......9606"
/db_xref="taxon:9606"
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/protein_id="CAD28501.1"
/db_xref="GI:19584420"
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mol_type="mRNA"
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Pred. No. 2.9e-104;
0; Mismatches 18;
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AY325114
AY325114.1 GI:32967226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tang,Y.T., Emtage,P., Funk,W., Hu,T., Arterburn,M.,
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Location/Qualifiers
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                                                        CGCAACAGGCAACAAAATTAAGACCACGAGAATTCACCCAAGAACCTAACAGAAGCATTT 797
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eviaahrccnknribersqtvkcsclpgkvagttrnrpscvdasivigkwwcemepcl
egeecktlpdnsgwycatgnkikttrihprt"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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	Center: University of Washington Genome Center Code: UMGC  Web Site: http://www.genome.washington.edu Contact: uwgchtgs@u.washington.edu Drafting Center: BcM	COMMENT On Sep 13, 2001 this sequence version replaced gi:15138904.	enter, University of	Submitted (16-JUN-2001) Genome Center, University of Box 352145, Seattle, WA 98195, USA 3 (bases 1 to 137703) 3 (bases 1 to 137703) Gloudy, James, R.A., Raymond, C. Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Raymond, C. Clordenico, T. and University of Condension of Sand University of Sand Condension of Sand Co	Kaulk.K., Oison,M.V., Kaymono,C., Ciendenning,J., Iv Haugen,E.D. Direct Submission	03)	1 (bases Kaul,R.K., Clendennin	ORGANISM Homo supreme (Transmir)  DRGANISM Homo sapiens  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	RESULT 5 ACC92036/C ACC92036 A	DY 798 GTGGTAAGGAA 812
nce quality program. ced to quality zero. have less than rally visible from the	<u>5</u> .	513	0	y or wasningcon, ond,C.,	, ,	)	ond, C.,	Eutele; Homo.	PRI 13 seque	

quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

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Insert size: 158080; sum-of-contigs Quality coverage: 11.0x in Q20 bases; sum-of-contigs		ATTTAA 120        ATTTAA 10112	TTATCTCCCCATCACTTCAAAGGTCTCGTCAGGCAGAGGTGACGCCAGGAGATGATTTAA 	GGCAGAGGTO	AAAGGTCTCGTCA              AAAGGTCTCGTCA	CATCACTTC	61 TTATCTCCC	৳ ৺
Assembly program: Phrap; version 0.990319 Consensus quality: 158072 bases at least Q40 Consensus quality: 158080 bases at least Q20 Consensus quality: 158080 bases at least Q20	37 W	TGCACA 60        GCACA 10172	CACTGGAGTGGGGATGGTCCATCGGCAACTATAAACTGATTCTCATCAGGAAACTGCACA	TAAACTGATT          TAAACTGATT	CACTGGAGTGGGGATGGTCCATCGGCAACTATAAACTGATT	GGGGATGGT	1 CACTGGAGT          10231 CACTGGAGT	ਲੇ ਨ
Sequencing vector: plasmid; 46% of reads Sequencing vector: M13; LU8821; 54% of reads Chemistry: Dye-terminator Big Dye; 99% of reads Chemistry: Dye-primer Bodipy; 1% of reads		Gaps 1;	Length 137703; Indels 3;	; DB 9; .2e-87; es 2;	Score 368.8; DE Pred. No. 4.2e-8 0; Mismatches	45.4%; 98.7%; vative	Query Match 45.4%; Best Local Similarity 98.7%; Matches 383; Conservative	Z W Q
Center project name: chr-3 Center clone name: RP11-81N13 (bc0203)		1796	1823					
Drafting Conter: BCN  Project Information	-	4371						
Web site: http://www.genome.washington.edu Contact: uwqchtqs@u.washington.edu		4147	: :					
Center: University of Washington Genome Center Center Code: UWGC		2099						
COMMENT On Jan 25, Descrite, An 3022, Our COMMENT On Jan 27, 13178.		<800	585					
TITLE Direct Submission  GOURNAL Submitted (22-JAN-2003) Genome Center, University of Washingt		879	888					
Saenphimmachak, C., Buckley, D., Kibukawa, M., Haugen, E.D.		<800	204					
REFERENCE 3 (bases 1 to 158080) AUTHORS Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,		879	799					
Submitted (28-DEC-2002) Genome Center, University Box 352145, Seattle, WA 98195, USA	Y	<800	464	826	821			
Xaul,R.K., Olson,M.V., Raymond,C. and F		4596	4592	5250	5322			
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Haugen, E.U. Direct Submission		<800	677	9605	9705			
		2830	2882	<800	443			
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ORGANISM HOMO SAPIENS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost		<800	12	< 800	419			
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9931	Db	<800	117	7421	7554	2727	2714	
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9991 TTTTTTTTAATCCTGATAAAGAAGATTGTTGGGAAGCTCTTTGAAAAAAAA	מֹם	<800	423	2796	2787	778	771	
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On Jan 22, 2003 this sequence version replaced gi:2/4131/8.	MMENT
Box 352145, Seattle, WA 98195, USA	
Submitted (22-JAN-2003) Genome Center, University of Washington,	JOURNAL
Direct Submission	TITLE
Saenphimmachak, C., Buckley, D., Kibukawa, M., kaymond, C. and Handen, B.D.	
Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., wu, Z.,	AUTHORS
3 (bases 1 to 158080)	FERENCE
Box 352145, Seattle, WA 98195, USA	
Submitted (28-DEC-2002) Genome Center, University of Washington,	JOURNAL
Direct Submission	TITLE
Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.	AUTHORS
2 (bases 1 to 158080)	FERENCE
Unpublished	JOURNAL
Direct Submission	TITLE
Haugen, E.D.	
Saenphimmachak, C., Buckley, D., Kibukawa, M., Raymond, C. and	
Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,	AUTHORS
1 (bases 1 to 158080)	FERENCE
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
Homo sapiens	ORGANISM
Homo sapiens (human)	URCE
HTG.	YWORDS
AC138390.2 GI:27819541	RSION
	CESSION
Homo sapiens chromosome 3 clone RP11-81N13, complete sequence.	FINITION
AC138390 158080 bp DNA linear PRI 22-UAN-2003	cus
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1225 1225 5520 5367 5619 5542	1784 1712 3204 3188 2712 2734		1413 3015 3023 1815 1	9934 9693 2083 2138 768 779	2003 2014 56 <800 509 <800	6850 6907 2016 1912 17081 17289	4027 3995 1207 1229 5523 5542	3 8768 3742 3737	6963 6907 3181 3188 92 <800	57 <800	2448 2480 680 <800 11041 10803	<800 3261	968 946 2196 2138 5429 5542	1505 1524 449 <800 4117 4117	<800 12792 1		8/68 /698 /651		SeqDerMap FngrPrnt SeqDerMap FngrPrnt SeqDerMap FngrPrnt	ECORI	between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.	are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies	vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp)	ragments with sequence-predicted fragments is given below.  The electronically-digested sequence consists of both insert and	This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest	Sequence Validation:	covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.	<pre>quality &gt;= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were</pre>	all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred	This sequence was finished as follows unless otherwise noted:	GenBank flat file format but are available as part of this entry's ASN.1 file.	1 error in 10,000 bp. Base-by-base quality values are not generally visible from the	All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than	This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.		5': RP11-79C12 (UWGC:bc0194) AC092036, 134230-bp overlap 3': RP11-89A12 (UWGC:bc0207) AC092416, 45454-bp overlap	
		242 <800	3363 3361						6636 6599	L	818 828	5322 5258	1548 1524	9705 9693	443 <800	3343 3361	419 <800	2611 2663	1691 1712	5781 5807	7332 7429	5348 5258	281 <800	4961 4996	7554 7429	1973 2014	2787 2820	. 893 946	3659 3686	1791 1712	715 <800	4504 4516	1739 1712	3219 3361	3448 3361	698 <800	1719 1712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
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Manmalia; Eutheria; Primates; Catarrhin; Yellouseria, Eutheria; Manmalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

Namizny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,
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Balbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D.,
Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P.,
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Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
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Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,
Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
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Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
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Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C.,
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Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J.,
Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens 3 BAC RP11-688P9 (Roswell Park Cancer Institute Human
BAC Library) complete sequence.
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Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Moore, S., Mosgan, M., Moorish, T., Morris, S., Moser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Nickerson, E., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Pare, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L. L., Quiles, M., Ren, Y., Rives, M., Rojab, R., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Soott, G., Shen, H., Shooshtari, N., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Tang, H., Tansey, J., Taylor, C., Vera, V., Villalon, D., Vinson, R., Wang, G., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlingson, A., Wooden, S., Williams, G., Wu, Y., Wu, Y., Mu, Y., Mu, Y., Mu, Y., Mu, Y., Mun, Y., Zorrilla, S., Naylor, S.L., Weinstock, G. and Gibba, P. Zhou, J., Zorrilla, S., Naylor, S.L., Weinstock, G. and
                                                                                                                                                                                                                                                                                                             Submitted (13-FEB-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA [bases_1 to 187748]
Submitted (19-MAR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 4 (bases 1 to 187748)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 187748)
Worley, K.C.
Direct Submission
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Direct Submission
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JOURNAL REFERENCE AUTHORS TITLE

JOURNAL

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COMMENT

REFERENCE AUTHORS TITLE JOURNAL Submitted (20-MAR-2003) Human Genome Sequencing Center, Depa of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA On Max 20, 2003 this sequence version replaced gi:29123832.

INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email Direct Submission Worley, K.C.

Department

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing. Overlapping clones are noted at the beginning and

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome of a local database that includes entries local mapping efforts. Res. 7:541-550) searches from dbSTS, GDB, and

Repeats are identified using RepeatMasker (A. Smit and P. Green

unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the SEQUENCING READ COVERAGE: Sequencing is completed to a minimum annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality error rate less than 1 per 10,000 bases.

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FEATURES
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/rpt family="MLTIC"
complement(8992..9346)
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467. .691
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13267...1
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/chromosome="3"
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|mol_type="genomic DNA"
    /rpt_family="L1MA8"
complement(14577. .14883)
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12516. .1
                                                                                                                                                                                                                                                                                                                      /rpt_family="L1ME3B"
0148. .joi77
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                                                                  'rpt_family="(CAA)n"
13539. .13620
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1 (bases 1 to 247515)
Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
Anyalebechi,V., Acyagi,A., Ayodeji,M., Baca,E., Baden,H.,
                                                                                                                             AC116080.4 GI:23664937
HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_ENRICHED
Rattus norvegicus (Norway rat)
                                                                               Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                              AC116080
                                                                                                                                                                                                          AC116080 247515 bp DNA linear HTG 11-OCT-2002
Rattus norvegicus clone CH230-40C18, *** SEQUENCING IN PROGRESS
                                                                  Rattus
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17996. .18710
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/rpt_family="AluSx"
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complement(19617. .19914)
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15580. .16677
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15436. .15578
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.7841. .17993
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98.7%;
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Pred. No. 4.2e-87;
0; Mismatches 2
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Biswalo, K., Blatz, J., Blankenburg, K., Bythstead, M., Bernmed, F., Biswalo, K., Blatz, J., Blankenburg, K., Byth, P., Brown, M., Bryant, N., Bhhay, C., Burch, P., Burrell, K., Calderon, E., Chu, J., Cardenas, V., Carter, K., Cavazos, I., Coesas, H., Center, A., Chu, J., Clacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chu, J., Cleveland, C., Cookrell, R., Cox, C., Coyle, M., Gree, A., Dryouza, L., Davis, C., Deramo, C., Ding, Y., Dinh, H., Divya, K., Delgado, O., Denson, S., Dunn, A., Durbin, K., Duvall, B., Zaves, K., Egan, A., Escotto, M., Edgene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Elgen, C., Evals, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Blagene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Glar, R., Garcia, A., Garner, T., Garca, M., Gebrere, R., Gall, R., Grady, M., Glerre, W., Gewara, W., Gunarathe, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Hernandez, S., Finley, M., Hadin, S.L., Hodgson, A., Hogues, M., Hernandez, S., Hallan, S., Haldan, S.L., Hodgson, A., Hogues, M., Hernandez, S., Finley, S., Haldan, S.L., Hodgson, A., Hogues, M., Hernandez, S., Lope, M., Garcia, M., Garrie, W., Garcia, M., Marcia, M., Marcia, M., Marcia, M., Marcia, M., Marcia, M., Marcia, M., Marcia,
                Submitted (11-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Oct 10, 2002 this sequence version replaced gi:21736969. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (24-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 247515)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Worley, K.C.
Direct Submission
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TGAATGAACCCGATGTCTTTTTTTTTACTGTGGAAATAGGATCGGAAGAGAGAACATTT 240
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misc_feature
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                                                                                                                                                                                                                                                                                                                                 Similarity
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.)

NOTE: This is a "working draft' sequence. It currently

consists of 1 contigs. Gaps between the contigs

are represented as runs of N. The order of the pieces
is believed to be correct as given, however the sizes
of the gaps between them are based on estimates that have
provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 247515: contig of 247515 bp in length.
                                             AGGTGAAAATGACAAGGTTTCCACCCCTCAAACCTTGGCTCCTTTTCTGACAATACAGTC 180
                                                                                               TTAGCTCACCATCACTTCAAAGGTCTCGTCAGACAGAGGTGACGCCAGGGGATGATTTAA
                                                                                                                                                                                                      CACTGGAGTAGGGATGGTCTGTCCGTGGCTATAAACTGCTTCTCTTCAGGAAAACT--ACA 141579
AGGTGAACATGACAAGGTTTCCACCCCTCAAACCTTGGTTCCTTTTCTGACAATACAG-- 141461
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Center clone name: CH230-40C18
Center clone name: CH230-40C18
Center summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 22334 bases at least Q40
Consensus quality: 231595 bases at least Q20
Consensus quality: 231595 bases at least Q20
Consensus quality: 232872 bases at least Q20
Estimated insert size: 236904; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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clone_end:T7"_
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245971. .247515
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243698. .245700
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/note="clone_boundary
clone_end:T7
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Pred. No. 3.2e-46;
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                                                                                                                         Submitted (25-NOV-2003) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, On Sep 6, 2003 this sequence version replaced gi:21735140.
                                                                                                                                                                                                                                                                                                                                              Parkway, St. Louis, MO 63108, USA
4 (bases 1 to 193027)
McPherson, JD. and Waterston, R.H.
Direct Submission
Submitted (12-UTL-2002) Genome Sequencing Center, 4444 Forest
Parkway, St. Louis, MO 63108, USA
5 (bases 1 to 193027)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 (bases 1 to 193027)
MCPherson, J.D. and Waterston, R.H.
Direct Submission
Submitted (08-APR-2002) Genome Sequencing Center, 4444 Forest Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 193027)
Swearengen-Shahid, S., Kozlowicz, A. and Schatzkamer, K.
The sequence of Mus musculus BAC clone RP23-41072
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC117234 193027 bp DNA linear ROD 25-NO Mus musculus BAC clone RP23-41002 from chromosome 6, complete
                                                                                                                                                                                                                                                                  Submitted (06-SEP-2003) Genome Sequencing Center, 4444 Forest Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                           Wilson, R.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing of Mus musculus Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence.
                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                              Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTTTTTT-----AATCCTGATAAAGAA--GATTGTTGGGAAGCTCTTTGAAAAAAA
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                                                                                                                                                                                                                                              (bases 1 to 193027)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 193027)
Contact: submissions@watson.wustl.edu
------ Summary Statistics
Center project name: M_BA0410J02
                                                              Web site: http://genome.wustl.edu
                                                                                   Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GI:34495048
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chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu

SOURCE INFORMATION:

The RPCI-23 BAC Library has been constructed by Kazutoyo Osegawa and Minako Tateno in the laboratory of Pieter de Jong (http://www.chori.org) from female C57BL/6J mouse kidney and/or brain genomic DNA. The clone and detailed information can be obtained from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org

FEATURES repeat\_region NEIGHBORING SEQUENCE INFORMATION:
This sequence is the entire insert
Location/Qualifiers /rpt\_family="MIR" 8988. .9064 /rpt\_family="L1" 4708. .4969 9600. .9719 /rpt\_family="MaLR" 11657. .11695 /rpt\_family="ERVK" 9260. .9476 /rpt\_family="B4" 528. ..737 /rpt\_family="L1" 129. .. 197 /rpt\_family="L2" 11697. .12125 /organism="Mus musculus" /mol\_type="genomic DNA" /db\_xref="taxon:10090" /chromosome="6" /rpt\_1 'rpt\_family="B4" rpt\_family="MER2\_type" 2124. rpt\_family="MaLR" rpt\_family="MaLR" rpt\_family="RMER15" rpt\_family="ID" clone\_lib="RPCI-23" clone="RP23-410J2" .193027 \_family="L1" \_family="L1" \_family="B4" \_family="MER1\_type" \_family="L1" tami .3988 6355 12849 12182 lly="L1" 얁 the clone.

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate

repeat\_region

/rpt\_1 12860

family="L1"

rpt\_family="L1"

repeat\_region repeat\_region repeat\_region repeat\_region

/rpt\_family="L2" 24937. .25060

family="B4" \_family="B4" family="L1" family="L2" \_family="MIR" \_family="MIR"

21506

.24434

repeat\_region repeat\_region

rpt\_family="L2" 16793. .16958 /rpt\_family="L1" 15767. .15806 /rpt\_family="L1" 14712, .15744

17198

repeat\_region

repeat\_region repeat\_region

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REFERENCE
AUTHORS
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source
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Best Local Similarity 98.9%; Pred. No. 9.4e-39;
Matches 187; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 309; Conservative
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101018 AAGCATTCTCTTTGÀÀÀÀATCTCAGÀÀCTGTGGCÀCÁGÀTGGÁTTTTÀÀÀÀAAGTGTTAGC 100959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101253 TAGCTCACCÁTCACTTCAAAGGTCTCGTCAGACAGAGGTGACGCCAGGGGATGATTTAAA 101194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101135 GAACGAGCCCAACGTC---TTCACAACTGTGGAAACGGGACTGGAAGAGAAAAGCTTGCC 101079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101311 ACTGGAGTAGGGATGGTCTGTCCGTGGCTATAAACTGCTTCTCATCAGGAAACT--ACAT 101254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               331
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181 TGAATGAAC 189
                                                                                                                                           61 TTATCTCCCCATCACTTCAAAGGTCTCGTCAGGCAGAGGTGACGCCAGGAGATGATTTAA 120
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                                                                                                                                                                                                 73 CACTGGANNGGGGATGGTCCATCGGCAACTATAAACTGATTCTCATCAGGAAACTGCACA
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                                                                                                                                                                                                                        1 CACTGGAGTGGGGATGGTCCATCGGCAACTATAAACTGATTCTCATCAGGAAACTGCACA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AX896885 261 bp DNA
Sequence 12748 from Patent EP1033401.
AX896885
AX896885.1 GI:40051769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dumas Milne Edwards, J.B., Duclert, A. and Giordano, J.Y. Expressed sequence tags and encoded human proteins Patent: EP 1033401-A 12748 06-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                          AGGTGAAAATGACAAGGTTTCCACCCCTCAAACCTTGGCTCCTTTTCTGACAATACAGTC 180
                                                                                                                    TTATCTCCCCATCACTTCAAAGGTCTCGTCAGGCAGAGGTGACGCCAGGAGATGATTTAA
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                                       AGGTGAAAATGACAAGGTTTCCACCCCTCAAACCTTGGCTCCTTTTCTGACAATACAGTC
                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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Pred. No. 1.4e-39;
0; Mismatches 68;
                                                                                                                                                                                                                                                                                                                    Length 261,
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repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region

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fami

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.33421 .33150

/rpt\_family="B4" 37402. .37493

\_fami

ramily="B2" . .38019

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\_family="ERVK"

.38425

.ly="Alu"

\_fami

ly="Alu"

.37439

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family="MIR"

. 25973

\_family="ID"

.31684

/rpt\_family="L2" 32532. .32617

\_family="MER1\_type"

repeat\_region

/rpt\_f 41548.

\_family="MaLR" \_family="ERVK"

.41406 .40501

/rpt\_family="MaLR" 42486. .42881

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/rpt\_\_..... 43220. ..43399 /rpt\_family="ERVK" /rpt\_fa4558

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fami

ly="L1"

.38609

LY="ERVK"

38426. /rpt\_fami 38503. .3

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REFERENCE
AUTHORS
TITLE
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BD032418
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Best Local Similarity
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OS Homo
PN JP 20
PD 02-OC
PF 24-FE
PR 26-FE
PR JEAN I
PI JORDAN
PC C12N15
                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                               73
                                                                                       173288 bp DNA linear PRI 07-FEB-
Homo sapiens chromosome 3 clone RP11-253K11, complete sequence.
AC104167 AC040915
AC104167.2 GI:18583922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 261)

Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.

Sequence tag and encoded human protein

Patent: JP 2001269182-A 8664 02-OCT-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              유
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 173288)
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                                               Homo sapiens (human)
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TGAATGAAC 261
                                                                                                                                                                                                                                                                                                                                                                                           TTATCTCCCCATCACTTCAAAGGTCTCGTCAGGCAGAGGTGACGCCAGGAGATGATTTAA 120
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                                                                                                                                                                                                                                                              TGAATGAAC 189
                                                                                                                                                                                                                                                                                                AGGTGAAAATGACAAGGTTTCCACCCCTCAAACCTTGGCTCCTTTTCTGACAATACAGTC
                                                                                                                                                                                                                                                                                                                             AGGTGAAAATGACAAGGTTTCCACCCCTCAAACCTTGGCTCCTTTTCTGACAATACAGTC 180
                                                                                                                                                                                                                                                                                                                                                                                                                           CACTGGANNGGGGATGGTCCATCGGCAACTATAAACTGATTCTCATCAGGAAACTGCACA 132
                                                                                                                                                                                                                                  TGAATGAAC
                                                                                                                                                                                                                                                                                                                                                               TTATCTCCCCATCACTTCAAAGGTCTCGTCAGGCAGAGGTGACGCCAGGAGATGATTTAA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
JP 2001269182-A/8664
02-OCT-2001
24-FEB-2000 JP 2000118773
26-FEB-1999 US 60/122487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C12P21/02, C12P21/08, C12Q1/68//G06F17/30, C12N15/00, C12N5/00, PC
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JEAN BAPUTIST DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
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/db_xref="taxon:9606"
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Location/Qualifiers
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mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 187; DB 6;
Pred. No. 9.4e-39;
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l human
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SeqDerMap FngrPrnt

HindIII
SeqDerMap FngrPrnt

SeqDerMap

FngrPrnt

BglII

fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

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JOURNAL
REFERENCE
AUTHORS
TITLE
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                                                                                               This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Overlapping Sequences:
5': RP11-306N11 (UWGC:bc0642) AC104443
3': RP11-40E22 (UWGC:bc0611) AC046199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (07-FEB-2002) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA
On Feb 7, 2002 this sequence version replaced gi:17352431.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z., Saenphimmachak,C., Phelps,K.A., Raymond,C. and Haugen,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (05-DEC-2001) Genome Rox 352145, Seattle, WA 98195,
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Saenphimmachak,C., Phelps,K.A., Raymond,C. and Haugen,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
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3 (bases 1 to 173288)
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Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D
                               Sequence Validation:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence Quality Assessment:
                                                                                                                                                                                                                                                                                                                                                                        This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name: chr-3
Center clone name: RP11-253K11 (bc0635)
Center clone name: RP11-253K11 (bc0635)
Center clone name: RP11-253K11 (bc0635)
Sequencing vector: unknown; 50% of reads
Sequencing vector: plasmid; 50% of reads
Chemistry: Dye-terminator ET; 80% of reads
Chemistry: Dye-terminator Big Dye; 20% of reads
Chemistry: Dye-terminator Big Dye; 20% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 17303 bases at least Q40
Consensus quality: 173181 bases at least Q20
Insert size: 173288; sum-of-contigs
This sequence has been validated by Multiple Complete Digest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drafting Center: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.genome.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center Code: UWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality coverage: 10.4x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: University of Washington Genome Center
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23 <800 271 <800 09 <800 1694 1730 09 4800 3465 3506 04 7888 3465 3506 04 2013 2043 20 <800 2013 2043 20 2869 2895 1386 2860 5437	1459     1386     1688     1730     3256     3246       1101     1116     2177     2209     2895     2959       517     <800     3062     3069     609     <800       2166     2129     6219     6140     1121     1116       2429     2394     7221     7163     3560     3591       2440     2538     10686     10536     7604     7678	1430 1386 1386 1386 1386 1386 1386 1386 1386	8884 3187 3244 5382 6545 6545 6545 6545 6545 6545 6545 654
RESULT 13 AC112214 AC112214 AC112214 AC112214 AC112214 ACCESSION Homo sapiens chromosome 3 clone RP11-649F12, complete sequence. ACCESSION AC112214 VERSION AC112214 VERSION HTG. KEYWORDS HTG. SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Qy 499 CCAGAAGGAGGACGTGTGAAGTGATAGCAACACCGATGTTGTAACAAGAATCGCATT 558	3585 3775 6930 6545  601 <800 1414 1429  2655 2672 6608 6545  2683 2872 4638 4668  1598 1568 3497 3506  1244 1213 673 6545  1244 1213 673 6545  1244 1213 673 6545  13494 3531 3037 3069  milarity 100.0%; Pred. No. 1.5e-27; Indels Conservative 0; Mismatches 0; Indels	4677     4625     945     883     1128       1141     1116     562     <800

r.			REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL COMMENT
Sequence Validation: This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.  SeqDerMap FngrPrnt SeqDerMap FngrPrnt SeqDerMap FngrPrnt SeqDerMap FngrPrnt SeqDerMap FngrPrnt	mment:  nnotated with sequence the phrap assembly pro- asses have been reduced 40 are expected to have values are not generall mat but are available file.  file.  shed as follows unless or double-stranded or se covered by high qualit empt was made to resolu- ressions and repeats; ressions and repeats; le plasmid subclone or n mbly was confirmed by 1	Center: University of Washington Genome Center Center: University of Washington Genome Center Center Code: UWGC Web site: http://www.genome.washington.edu Contact: uwgchtgs@u.washington.edu Contact: uwgchtgs@u.washington.edu Center project Information Center project name: chr-3 Center project name: RP11-649F12 (bc0666)  Center Clone name: RP11-89 favor reads Center clone name: RP11-649F12 (bc0666)  Center Clone name: RP11-89 favor reads Center Clone name: RP11-89 favor reads Center Clone name: RP11-89 favor at least Q40 Consensus quality: 173970 bases at least Q40 Consensus quality: 173970 bases at least Q20 Consensus quality: 173990 bases at least Q20 Consensus quality: 173990 bases at least Q20 Consensus quality: 173990 bases at least Q20 Consensus quality: 173970 bases at least Q20 Consen	1 (bases 1 to 173990)  Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z., Saenphimmachak, C., Phelps, K.A., Raymond, C. and Haugen, E.D. Direct Submission Unpublished 2 (bases 1 to 173990)  Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D. Direct Submission Submitted (20-FEB-2002) Genome Center, University of Washington, Submitted (20-FEB-2002) Genome Center, University of Washington, Submitted (20-FEB-2002) Genome Center, University of Washington, Saenphimmachak, C., Phelps, K.A., Raymond, C. and Haugen, E.D. Direct Submission Submitted (29-MAR-2002) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA On Mar 29, 2002 this sequence version replaced gi:18767513.
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2024 2024 2024 2024 2024 2024 2024 2024	3738 1378 1378 1378 1378 1 1378 1 12901 1 1290	2108 791 399 2338 2338 2558 12241 12241 12241 3573 3795 3795	176
2814 2002 2145 6067 <800 11369 9507 2145	3717 1368 2904 3497 <800 1216 2553 1557	2145 813 4106 2442 <800 2442 12505 12505 3584 2686 3976	8565 <b>8</b> 800 <b>7</b> 607 <b>7</b> 607 <b>2</b> 686 <b>8</b> 565 <b>8</b> 565
54223313131661 2212313131661	3199 954 954 1778 1454 1677 1677 1677 1677 1677 1780	3467 1208 1208 862 1928 11928 11992 11436 1436 301 301 436 2042	6884 100 100 100 100 100 100 100 10
7019 <800 849 1186 2409 2307 <800	3197 979 1745 1398 <800 1612 5103 4362	3391 1186 849 2033 11986 7019 1398 <8800 <8800 2033 1186	7019 2033 9146 <800 979 6122
983 3647 6619 8344 4609 4609 849	388 2059 2059 3684 2170 2170 2765 6731	أها أسا اسابابانيا اسا	3687 6382 512 512 11952 11952
3659 6611 8266 4499 2570 2807	<pre>&lt;800 2189 3659 2189 2189 3027 2770 6611 &lt;800 3478</pre>	8266 <800 5476 1690 1690 3129 <800 3478 956	3659 6611 <800 <800 12067 4499 <800

RESULT 14 AY325123 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	Qy Db 12 Qy Db 12	Query Ma Best Lou Matches Qy Db 12		
<u>s</u> 4	559 GAGGAGCC         124342 GAGGAGCC 619 AGAAACCC         124402 AGAAACCC	Query Match 17.9%; Best Local Similarity 100.0%; Matches 145; Conservative 499 CCAGAAGGAGGGACGTGTG	2248 883 4124 4124 819 3304 1141 1420 1440 1404 20 7691 109 1123 22429 2440 2429 2429 2168 517 1101 1459 314	9522
AY325123 901 k Mus musculus TAFA4 mRNA, compl AY325123 AY325123.1 GI:32967244 Mus musculus (house mouse) Mus musculus Eukaryota; Metazoa; Chordata;	GAGGAGCGGTCACAAACAGTRAAGTG 	17.9%; EY 100.0%; EYALIVE ( HAGGACGTGTGI HAGGGACGTGTGI JAGGGACGTGTGI	2261 898 4106 813 3334 1109 4566 1368 1368 1368 2400 2442 2553 2145 2145 2145 2800	9507
901 b compl e)	AAAGTGTTCCTG   AAAAGTGTTCCTG   AAAAGTGTTCCTG   CGATG 643	Score 145; DB 9; 1 , Pred. No. 1.5e-27; , mismatches 0; O; Mismatches 0;  JAAGTGATAGCAGCACCGA'	4124 4124 1371 2971 1023 588 1612 269 2160 2160 2160 2160 3272 3272 3272 3272 3272 3272 3272 327	1107
ete cds. Craniata; Ver	FCTACCTGG	DB 9; Ler5e-27; s 0; :ACACCGATGT		1112
linear ROD	GAGGAGCGGTCACAAACAGTAAAGTGTTCCTGTCTACCTGGAAAAGTGGCTGGAACAACA	17.9%; Score 145; DB 9; Length 173990; imilarity 100.0%; Pred. No. 1.5e-27; Indels 0; Gaps; Conservative 0; Mismatches 0; Indels 0; Gaps CCAGAAGGAGGACGTGTGAAGAATCGCATT[	1120 1189 9661 525 315 4194 4194 4194 562 945 945 1956 3465 3465 10687 7222 6205 3064 3064 4188	484
ROD 23-JUL-2003	ACAACA 618         ACAACA 124401		1122 1920 9610 <800 4146 <800 956 5476 22869 2031 3478 11690 10712 7247 6158 3027 2189	<800
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REFERENCE AUTHORS TITLE JOURNAL	AKOSTE 15 AKOST890 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM		UTHORS UTILE COURNAL TOURNAL TOURNAL COUNTHORS COURNAL	
Eukaryota; Meta; Mammalia; Euthes 1 Tashiro,H., Yama Fukuzumi,Y., Fu Nakagawa,K., Mii Irie,R., Otsuki, Irie,R., Otsuki, Kawakami,B., Nao NEDO human cDNA Unpublished	AK057890 Homo sapiens cDN AK057890 1 GI:1 cligo capping; i Homo sapiens Homo sapiens	520 CTTGGAAGGAGAGG 747 CAACAAAATTAAGI 747 CAATAAAGTCAAAG	Tang, Y.T., Emtagy TAFA: A Novel Sey PAFA: A Nov	Mammalia; Euthe 1 (bases 1 to

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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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JEDCKVLPDSSGWSCSSGNKVKTTKVTR"
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TUN-2003) Biology Research, Nuvelo, 675 Almanor
Lle, CA 94085, USA
on/Qualifiers
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age, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHATGCCTCCATAGTGATTGGGAAAATGGTGGTGAGATGGAGCCTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.9%; Score 137.4; DB 10; Length 901;
57.0%; Pred. No. 1.5e-25;
1ve 0; Mismatches 96; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nism="Mus musculus"
YPe="mRNA"
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ge,P., Funk,W., Hu,T., Arterburn,M., Park,B. and
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                                                                                                               JACCACGAGAATTCACCCAAGAACCTAACAGAAGCATTT
                                                                                                                                                                                                                         ;GACTGTAAAGTGCTTCCAGACTCTTCGGGTTGGTCCTGTAGCAGTGG
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Best Local Similarity 70.4%;
Matches 183; Conservative (
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MEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction and 5'-end one pass sequencing: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; 3'-end one pass sequencing: RAB; clone selection for full insert sequencing: RAB and Helix Research Institute.
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Sugano, S. and Suzuki, Y.
Direct Submission
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/note="cloning vector: pME18SFL3"
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 US-09-620-312D-225
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ATCACCTGCACA	16.2%; ity 63.1%; servative	apiens . (596)		Yonghong Yonghong Jian-Rui Ping Unging Unging Dunrui Zhiwei EC, Radoje T	ication US/( N: N: Y: Tom Y: Tom i, Vinod i, Vinod i, Jie Feiyan Feiyan Feiyan Fon Fon Rong Oing A.	2 2 2 2 1000 4 2 2 1000 4 4 2 2 1000 4 4 4 1000 1 4 1000 1 4 1000 1 4 1000 1 4 1000 1 4 1000 1 4 1000 1 4 1000 1 4 1000 1 4 1000 1 4 1000 1 4 1000 1 4 1000 1 4 1000 1 4 1000 1 4 1000 1 4 1000 1 4 1000 1 4 1000 1 4 1000 1 4 1000 1 4 1000 1 4 1000 1 4 1000 1 4 1000 1 4 1000 1 4 1000 1 4 1000 1 4 1000 1 4 1000 1 4 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 1000 1 10000 1 10000 1 10000 1 10000 1 1000 1 1000 1 1000 1 1000 1 1000 1	571 3867
CASCATCACCTGCACAGACCAGAAGGAGGGACGGTGTGAAGGTGATAAGCAGCACCACGAT 	Score 131.2; Pred. No. 9.8e 0; Mismatches		1des	D .	/09620312D	US-09-685-166A US-09-681-1638-1 US-09-326-529-1 US-09-326-5882-1 US-09-339-313-1 US-09-339-313-1 US-09-332-149A US-09-159-812-1 US-09-159-812-1 US-09-685-166A ALIGNMENTS	-08-858-207
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TELEPAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 218:
SEQUENCE CHARACTERISTICS:
LENGTH: 333 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: DOUBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Win95
SOFTWARE: Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,223
                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY JAGENT INFORMATION:
NAME: ISTAELSEN, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
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APPLICANT: buelert, Aymeric
APPLICANT: Lacroix, Bruno
TITLE OF INVENTION: 5' ESTS FOR SE
NUMBER OF SEQUENCES: 503
CORRESPONDENCE ADDRESS:
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                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
438 TGCAATGCTACTCTGCCATGGATCCCTTCAGC
                                                            240
                                                                                                                                       90;
                                                                                      TCAGAGAATGGCAATGGTCTCTGCGATGTCCTGGGTCCTGTATTTTGTGGATAAGTGCTTG 437
                                                            TTATAGAATGGCAATGGTCTCTGCGATGTCCTGGGTCCTGTATTTGTGGATAAGTGCTTG 299
                                                                                                                                     Conservative
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identity 99
region 54..214
id T80337
                                                                                                                                                                                                                                                                                                                                                                  identity 100 region 1..82 id HSCOCF041
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identity 100
region 213..272
id T80337
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entity 94
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                                                                                                                                     Score 88.8; DB 3;
Pred. No. 2e-18;
0; Mismatches 2
                       469
                                                                                                                                       2
                                                                                                                                                                          Length 333;
                                                                                                                                       Indels
                                                                                                                                     0
                                                                                                                                     Gaps
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CLASSIFICATION: ATTORNEY/AGENT INF

APPLICATION NUMBER: FILING DATE:

ZIP: 92101-3505 COUNTRY: CITY: San Diego

California

USA

STREET: ADDRESSEE:

501 West Broadway

Knobbe,

MOLECULE TYPE: CDNA
ORIGINAL SOURCE:

TOPOLOGY:

LINEAR

FEATURE:

TISSUE TYPE: ORGANISM:

Homo Sapiens E: Brain

NAME/KEY: other
LOCATION: 32..331
LOCATION: 32..331
LOCATION: METHOD:
LOCATION: 1der
OTHER INFORMATION: 1der
OTHER INFORMATION: 1d R
OTHER INFORMATION: est

US-08-905-223-218

595

Sequence 218, Applica Patent No. 6222029 GENERAL INFORMATION:

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300 TGCAATGCTACTCTGCCATGGATCCCTTCAGC 331

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
                                                                                                                                                                                                                                                                                                                                                                                               IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                   Local Similarity
nes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                  CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TLE OF INVENTION: MBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENGTH:
                                      1269
                                                                                                      1329
                                                                                                                                                                     1389
                                                                                                                                                                                                                             599
                                                                                                                                                                                                                                                             479 AGCAGCATCACCTGCACAGACCAGAAGGAGGACGTGTGAAGTGATAGCAGCACACCGAT 538
 719 ACAATTCTGGATGGATGTGCGCAACAGGCAACAAAATTAAGACCACGAGAATTCACCCAA 778
                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
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                               GAAAAGTGGCTGGAACAACAAGAAACCGGCCTTCTTGCGTCGATGCCTCCATAGTGATTG 658
                                                                                                                                                             GTTGTAACAAGAATCGCATTGAGGAGCGGTCACAAACAGTAAAGTGTTCCTGTCTACCTG
                                                               GGAAATGGTGGTGTGAGATGGAGCCTTGCCTAGAAGGAGAAGAATGTAAGACACTCCCTG 718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FALKNER, F. G.
VENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                            larity 2.4%; Pred. No. 0.00039; Conservative 195; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                 5.7%; Score 46.4; DB 1; Length 7218; 2.4%; Pred. No. 0.00039;
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US-09-621-976-2813
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                                                                           NUMBER OF SEQ ID NOS: 19335
SOPTWARE: Patent.pm
SEQ ID NO 2813
LENGTH: 832
                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
                                                                                                                                                                                                                                                                            Patent No.
                                                                                                                                                                                                                                                                             Sequence 2813, Application US/09621976 Patent No. 6639063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                            APPLICANT: Jobert, S. APPLICANT: Giordano,
                                                                                                                                           TITLE OF INVENTION: ESTs and Encoded Human Proteins. FILE REFERENCE: GENSET.054PR2 CURRENT APPLICATION NUMBER: US/09/621,976 CURRENT FILING DATE: 2000-07-21
FEATURE:
NAME/KEY: CDS
LOCATION: 235..399
                                             TYPE: DNA
ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177
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                                             sapiens
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CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 2813
LENGTH: 832
                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2813, Application US/09621976 Patent No. 6639063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: CDS
LOCATION: 235..399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LE REFERENCE: GENSET.054PR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 TTAAAGGTGAAAATGACAAGGTTTCCACCCCTCAAACCTTGGCTCCTTTTCTGACAATAC 176
                                                                                                                                                                                                                                                                                 237 CATWCYWYWKYWKRMWSKTCWSGSRGGYMTSYTSTRSYSMYWASWMYTMCWWWGRWWSTY 178
                                                                                                                                                                                                                                                                                                                            57 CACATTATCTCCCCATCACTTCAAAGGTCTCGTCAGGCAGAGGTGACGCCAGGAGATGAT 116
                                                                                                                                  ATTTTTTTTTAATCCTGATAAAGAAGATTGTTGGGAAGCTCTTTGAAAAAAATT 292
WAWAMWRMWIMMMYYWYWRAMKRRWWWRKWRSWSWMWMAWGMIRWAARMWWRWY 2
                                                                                         RKKSYRTRCAWAYAWKTKRSYYWCWRWKWKRCMMMMMAMAYGKTMMMRACWKTRYWRW
                                                                                                                                                                                     WYMAWGKKWWRYATTWRRAMMWWWAAWTMMWYMWAWCMSSRGAAMYRRIMMWGYRYWW 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAACCTAACAGAAGCATTTGTGGTAGTAAAGGAA
                                                                                                                                                                                                                                                                                                                                                                             Conservative 119;
                                                                                                                                                                                                                                                                                                                                                                        5.5%; Score 44.4; DB 4;
11.4%; Pred. No. 0.00048;
vative 119; Mismatches 90;
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                                                                                                                                                                                                                                                                                                                                                                             90;
                                                                                                                                                                                                                                                                                                                                                                                                                      Length 832;
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US-09-621-976-2813

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US-09-370-807-1/c
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RESULT 7
US-09-921-259-1/c
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4.8%; Score 39; DB 4; Length 832
Best Local Similarity 10.4%; Pred. No. 0.025;
Matches 33; Conservative 156; Mismatches 126; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09370807 Patent No. 6297034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/370,807
CURRENT FILING DATE: 1999-08-09
EARLIER APPLICATION UNMBER: 60/096,225
EARLIER FILING DATE: August 12, 1998
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Microsoft Office 97
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 77; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Cahoon, Rebecca E.
APPLICANT: Falco, S. Carl
APPLICANT: Rafalski, J. Antoni
APPLICANT: Sakai, Hajime
TITLE OF INVENTION: N-End Rule Pathway Enzymes
FILS REFERENCE: BB-1199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 2060
                                                                                            1938
                                                                                                                                                                                                                                                                         2058
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               256 TAAAGAAGATTGTTGGGAAGCTCTTTGAAAAAAATTTTAAATTGTGGCACAGATGGATT 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 KYTTWYAKCWTKWKWSWSYWMYWKWYYMKTYWRWRRKKKKAWWKYWKTWTWWYWRYAMWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTTGTGCAATGCTACTCTGCCATGGATCCCTTCAGCACACTTTCCAGCAGCATCACCTGC 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTTCAGAG--AATGGCAATGGTCTCTGCGATGTCCTGGGTCCTGTATTTGTGGATAAGTG 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYKKKAMCRIKIKKKKKKGYMWMWYWGWRRSYMAMWIRIWIGYAYYRSMMYWWRYRCWKK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WKRWWWCWARMYRYSTG 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KAYYRKTTCYSSKGWTWWKRWKKAWTTWWWKKTYYWAATRYWWMMCWTKRWRASWWYCWW 186
                                                                                                                                                                                 GTTCACAACATTGCTATTGCCAACATTGTCAGACCATTCAAAGGAAGAATACATGAATCT 1939
                                                                                                                                                                                                                         TTGTGGCACAGATGGATTTTAAAAAGTGTTAGATCTTTCCAATGAACACTAATAGAGTAC 357
                                                                                                                                                                                                                                                                                                                   TTTTTTTTTAATCCTGATAAAGAAGATTGTTGGGAAGCTCTTTGAAAAAAATTTTAAA 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CMMRRKYAGKSKTSYKSMWMCWTRSWKYCYTKARWTGYYCYRKGGMWGKRGRWYASKKYM 306
                                                                                          TCTTTGCAGAGTTTTTTTTTT 1918
                                                                                                                                                                                                                                                                         TTTTTTTTTTTTTTTGTAAAAAAGATATGTAAAATGTCCATTAACCAAAAACTTATGG 1998
                                                                                                                                     TCTGCTCTTGGCTGGATTTTT 378
                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                 54.6%;
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                                                                                                                                                                                                                                                                                                                                                               Score 38.6; DB 3;
Pred. No. 0.057;
0; Mismatches 64;
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                                                                                                                                                                                                                                                                                                                                                                 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      Length 2060;
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APPLICANT: Falco, S. Carl
APPLICANT: Rafalski, J. Antoni
APPLICANT: Rafalski, J. Antoni
APPLICANT: Sakai, Hajime
TITLE OF INVENTION: N-End Rule Pathway Enzymes
FILE REFERENCE: BB-1199
CURRENT APPLICATION UNMBER: US/09/921,259
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 60/096,225
PRIOR APPLICATION NUMBER: 60/096,225
PRIOR FILING DATE: August 12, 1998
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Microsoft Office 97
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RESULT 8
US-08-454-097-11/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 2060
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 4.8%;
Local Similarity 54.6%;
les 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1998 GTTCACAACATTGCTATTGCCAACATTGTCAGACCATTCAAAGGAAGAATACATGAATCT 1939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION:
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                                                                                                                                                                                                                                                     1918
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US-08-454-097-11/c

US-08-454-097-11/c

Sequence 11, Application US/08454097

Patent No. 5686412

GENERAL INFORMATION:

APPLICANT: Hoekstra, Merl F.

TITLE OF INVENTION: Protein Kinases

NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:

NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:

NUMBER: 233 South Wacker Drive, 6300 Sears Tower

STREET: 233 South Wacker Drive, 6300 Sears Tower

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOTTWARE: PATENTION: 424

APPLICATION NUMBER: US/08/454,097

FILING DATE: 30-MAY-1995

CLASSIFICATION NUMBER: US/08/454,097

FILING DATE: 21-JAN-1994

APPLICATION NUMBER: US 08/008,001

FILING DATE: 21-JAN-1994

APPLICATION NUMBER: US 08/008,001

FILING DATE: 21-JAN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/008,001

FILING DATE: 21-JAN-1993

PRIOR APPLICATION NUMBER: US 08/008,001

FILING DATE: 21-JAN-1994

APPLICATION NUMBER: US 08/008,001

FILING DATE: 03-S68612and, Greta E.

NAME: No. 5686412and, Greta E.

REGISTRATION NUMBER: 35,302

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US-08-185-359-11/c
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; LOCATION:
US-08-454-097-11
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                                        APPLICATION NUMBER: US 08/008,001
FILING DATE: 21-JAN-193
PRIOR APPLICATION DATA:
APPLICATION DATA: US 07/728,783
FILING DATE: 03-JUL-191
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6060296and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/3185
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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nes 88; Conserv
                                                                                                                                                                                                                                                      FILING DATE
                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                           TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                  60606-6402
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nucleic acid
DEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                              233 South Wacker Drive, 6300 Sears
                              312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                USA
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Pred. No. 0.
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306 CAGATGGATTTTAAAAAGTGTTAGATCTTTCCAATGAACACTAAT 350
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; NAME/KEY:
; LOCATION:
US-08-185-359-11
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                                                                                                                                                                                                                                                                                           SEQ ID NO 19
LENGTH: 6866
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GENERAL INFORMATION:
                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: DE 10019058.8 PRIOR FILING DATE: 2000-04-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/204,708
CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: PCT/EP01/03971
PRIOR FILING DATE: 2001-04-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: by Assessing DNA Methylation
FILE REFERENCE: 5013.1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: OLEK,
                                                                                                                                                                                                              OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens
                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                    FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 2914 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2073
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                                        3859 GAAATAGATTAAATGTTTTTTAATAAGTAATTAGGTAAGTATATTTATATAATGGAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2193 TGAGTCAGCAAGGCATTTTTTGTTTTAAAAAAATCTCATTTCCTTACAGAAACAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241
                                                                        186 GAACCCGATGTCTTTTTTTTTACTGTGGAAATAGGATCGGAAGAGAGTAACATTTTTTT 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88,
                                                                                                                                    Similarity
TTAATCCTGATAAAGAAGATTGTTGGGAAGCTCTTTGAAAAAAATTTTTAAATTGTGGCA 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGCAÇAGATGGATTTTAAAAAGTGTTAGATCTTTCCAATGAAÇACTAATAGA 353
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                                                                                                                  Conservative
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51.5%;
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                                                                                                              Score 37; DB 4; Length 6866; Pred. No. 0.37; 0; Mismatches 80; Indels
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Pred. No. 0.22;
0; Mismatches
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; ORGANISM: Homo sapiens
US-09-673-395A-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION
APPLICANT: SPECHT
APPLICANT: HINZMAI
APPLICANT: SCHMIT
APPLICANT: PILARSI
APPLICANT: PILARSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-489-847-86
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SEQ ID NO 82
LENGTH: 2143
                                                    SOFTWALL SEQ ID NO 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 82, Application Patent No. 6620923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 4.5%;
Best Local Similarity 52.3%;
Matches 80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION: a APPLICANT: Rosen et al TITLE OF INVENTION: 98 Human Secreted Proteins FILE REFERENCE: PZ031P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 86, Application US/09489847 Patent No. 6476195
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-09-673-395A-82/c
TYPE: DNA
ORGANISM: Homo sapiens
-09-489-847-86
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CURRENT APPLICATION NUMBER: US/09/673,395A
CURRENT FILING DATE: 2000-10-17
NUMBER OF SEQ ID NOS: 637
                                                                                                                                                                                      EARLIER FILING DATE: 1998-08-12
EARLIER APPLICATION NUMBER: 60/
EARLIER FILING DATE: 1998-08-06
                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/489,847
CURRENT FILING DATE: 2000-01-24
EARLIER APPLICATION NUMBER: PCT/US99/17130
EARLIER FILING DATE: 1999-07-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: ROSENTHAL, ANDRE
                                                                                                                       EARLIER APPLICATION NUMBER: 60/095,455
EARLIER FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 376
                                                                                                                                                                                                                                                                       EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
EARLIER APPLICATION NUMBER: 60/095,486
EARLIER FILING DATE: 1998-08-05
                                                                                                      SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                     EARLIER APPLICATION NUMBER: 60/096,319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 344 CACTAATAGAGTACTCTGCTCTTGGCTGGATTT 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             736 GGAATACAATGGTTGTTTTATCATAGTGTACACATTTAGCTTGTGGTAAATGACTCACA
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SCHMITT, ARMIN
PILARSKY, CHRIST
DAHL, EDGAR
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Pred. No. 0.34;
0; Mismatches 73;
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US-09-439-313-351/c

Sequence 351, Application US/09439313 Patent No. 6329505

GENERAL

INFORMATION:

APPLICANT: Xu, Jiangchun APPLICANT: Dillon, Davin C. APPLICANT: Mitcham, Jennifer L.

APPLICANT:
APPLICANT:
APPLICANT:

Jiang Yuqui Reed, Steven G. Kalos, Michael

Harlocker, Susan Louise

APPLICANT:

Fanger, Gary Retter, Mark

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Best Local Sim:
Matches 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 6537773
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.1 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Fraser et al.
TITLE OF INVENTION: Nucleotide Sequence of the Mycoplasma Genitalium Genome, Fragments
Patent No. 6537773
                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: PB193P1
CUTRENT APPLICATION NUMBER: US/08/545,528D
CURRENT FILING DATE: 1995-10-19
PRIOR APPLICATION NUMBER: US 08/488,018
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: US 08/473,545
                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 1
                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Mycoplasma genitalium
                                                                                                                                                                                                                                                                                                                                                       ENGTH: 580073
502549 À 502549
                                                                         502609 AAAAAACAGAAGCTAAGATTTTCACAGAAAATTTTGTTTTTGCTGATGAAGTTGATATTA 502550
                                                                                                                                                 502669 TTATTTTTGCTGATCAAACAAAAAGAGAAGCAATTATTGGTGCTGGTTTAATGCTTATTA
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                                                                                                                                                                                                                           68;
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Pred. No. 8.8;
0; Mismatches
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Pred. No. 0.43;
0; Mismatches 73;
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APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yuqui
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
FILE REPERENCE: 210121.427C8
CURRENT APPLICATION NUMBER: US/09/352,616A
CURRENT APPLICATION NUMBER: US/09/352,616A
CURRENT FILING DATE: 1999-07-13
NUMBER OF SEQ ID NOS: 472
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 351
LENGTH: 472
TYPE: DNA
ORGANISM: Homo sapien
US-09-352-616A-351
                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Watches 79; Conserve
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APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TILE REFERENCE: 210121.427C9
CURRENT FILING DATE: 1999-11-12
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 351
LENGTH: 472
TYPE: Num
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 351, Application US/09352616A PATENT NO. 6395278
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan Louise
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ORGANISM: Homo sapien
-09-439-313-351
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                                         344 CACTAATAGAGTACTCTGCTCTTGGCTGGATTT 376
                                                                                                                                      284 AAAAAATTITTAAATTGIGGCACAGAIGGATTITAAAAAGIGITTAGATCTITTCCAAIGAA 343
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CAATAACAATGGCATTAAGGTTTGACTTGAGTT 54
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ilarity 51.6%;
Conservative
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Search completed: April 9,

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Job time : 99 secs

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Result
No.
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      1121
1221
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1541
    Score
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Match
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716
2 716
2 390
3 3673778
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2 16724
            9268
3673778
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                               498
10886
40862
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13511
           14 US-10-037-270-225
15 US-10-117-722-225
15 US-10-104-0472-925
14 US-10-312-841-1
14 US-10-311-455-1064
14 US-10-311-455-2046
15 US-10-311-455-253
16 US-10-311-455-253
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                                                                                                                                                          Description
Sequence 225, App
Sequence 225, App
Sequence 892, App
Sequence 1, Appli
Sequence 1064, Ap
Sequence 1045, Ap
Sequence 2018, Ap
Sequence 2145, Ap
Sequence 2746, Ap
Sequence 278, Appli
Sequence 278, Appli
Sequence 253, Ap
Sequence 1573, Ap
Sequence 27, Appli
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Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/US07 PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/US06 NEW PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US06 NEW PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US07 NEW PUB.seq:*

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6: /cgn2_6/ptodata/1/pubpna/US08 NEW PUB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US08 PUBCOMB.seq:*

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9: /cgn2_6/ptodata/1/pubpna/US09 PUBCOMB.seq:*

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14: /cgn2_6/ptodata/1/pubpna/US09C PUBCOMB.seq:*

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16: /cgn2_6/ptodata/1/pubpna/US10C NEW PUB.seq:*

17: /cgn2_6/ptodata/1/pubpna/US10C NEW PUB.seq:*

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17: /cgn2_6/ptodata/1/pubpna/US10C NEW PUB.seq:*

18: /cgn2_6/ptodata/1/pubpna/US0O NEW PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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RESULT 1 US-10-037-270. Sequence 22: Publication GENERAL INFO APPLICANT: APPL	 11112222222222222222222222222222222
	399,66 399,66 399,66 399,66 399,66 399,66 399,66 399,66 399,66
270-225  225, Application US/100: ion No. US20030104529A1 INFORMATION: NT: Tang, Y. Tom NT: Liu, Chenghua NT: Asundi, Vinod NT: Ren, Feiyan NT: Chen, Rui-hong NT: Wehrman, Tom NT: Xue, Aidong J. NT: Wang, Yonghong NT: Wang, Yonghong NT: Wang, Yonghong NT: Wang, Yonghong NT: Wang, Fing NT: Wang, Ping NT: Wang, Chawei INT: Wang, Chawei FILVENTION: No. US20030: FILVENTION NUMBER: US/0-110-01-01-01-01-01-01-01-01-01-01-01-0	44444444444444444444444444444444444444
lication US/1003 N: V: Tom Chenghua di, Vinod g, Jie Feiyan Rui-hong Cing A. Comphong Aidong J. Yonghong Aidong J. Yonghong Vunging Ping Vunging Ping Vunging Chiwei John Andoje T. No. US200301 NO. No. US200301 NO. Polypeptide 784C1P2B POlypeptide 784C1P2B ON: NO. WOMBER: US/1 NUMBER: 09/488 NUMBER: 09/488 Senes Version 1. Sapiens	111416 203934 203934 203934 203934 10716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 50716 5071
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US/10037270 4529A1  d  d  d  d  john je T. US/20030104529A1el Nucleic Acids WS20030104529A1el Nucleic Acids ypeptides ypeptides 2ER: US/10/037,270 02-01-04 02-01-04 02-01-04 03-01-21 04-25 04-25 09/488,725 01-21 04	US-10-311-455-262 US-10-221-613-19 US-09-873-367C-332 US-10-311-455-91 US-09-764-877-2455 US-10-311-455-975 US-10-311-455-975 US-10-311-455-758 US-10-311-455-758 US-10-311-455-3029 US-10-125-968-1355 US-10-125-968-1355 US-10-127-632-286621 US-10-027-632-286621 US-10-027-632-286630 US-10-10-605-212 US-10-108-605-212 US-10-114-55-136-28 US-10-231-455-136-28 US-10-231-455-139 US-10-239-676-28 US-10-239-676-28 US-10-239-676-28 US-10-239-676-28 US-10-257-166-58 US-10-257-166-58 US-10-257-166-59 US-10-257-166-59 US-10-257-166-59 US-10-257-166-59 US-10-257-166-59 US-10-257-166-59 US-10-257-166-59 US-10-257-166-37 US-09-814-353-13846
8 and	Sequence 262, App Sequence 19, Appl Sequence 91, Appl Sequence 186, App Sequence 2455, App Sequence 2455, App Sequence 275, App Sequence 758, App Sequence 758, App Sequence 758, App Sequence 2029, App Sequence 2135, App Sequence 2141, App Sequence 286621, Sequence 286621, Sequence 286629, Sequence 2167, App Sequence 217, App Sequence 218630, Sequence 217, App Sequence 218630, Sequence 218630, Sequence 217, App Sequence 218630, Sequence 217, App Sequence 218630, Sequence 217, App Sequence 218, Appl Sequence 318, Appl Sequence 38, Appl Sequence 37, Appl Sequence 38, Appl Sequence 37, Appl Sequence 38, Appl Sequence 37,

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CURRENT APPLICATION NUMBER: US/10/117,72:
CURRENT FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: 09/620,312
PRIOR FILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-07-19
PRIOR PILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1104
SOFTWARE: pt_FL_genes Version 1.0
SEQ ID NO 225
LENGTH: 716
TYPE: DNA
ORGANISM: Homo sapiens
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; LOCATION: (201)..(596)
US-10-037-270-225
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; NAME/KEY: CDS
; LOCATION: (201)..(596)
US-10-117-722-225
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Best Local Similarity
Matches 202; Conserv
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                                                                                                   Query Match
Best Local Similarity
Matches 202; Conserv
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APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
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TITLE OF INVENTION: No. US20030219744A1el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2BCIP
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                        ACCATCATAAAGCTCACCATGTTAAAACGGGAACTTGTGAGGTGGTGGCACTCCACAGAT 354
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                                                                                                   Score 131.2; DB 15;
Pred. No. 3.6e-27;
0; Mismatches 118;
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                                                     Sequence 1, Application US/10312841
Publication No. US20030186277A1
Publication No. US20030186277A1
GENERAL INFORMATION:
APPLICANT: Epigenomics AG
TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
FILE REFERENCE: E01/1208/WO
CURRENT APPLICATION NUMBER: US/10/312,841
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 892
LENGTH: 2390
TYPE: DNA
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Best Local Similarity
Matches 135; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: NO. US20030236392A1e1
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: HELIX RESEARCH INSTITUTE
LENGTH: 3673778
TYPE: DNA
ORGANISM: Artificial Sequence
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o. US20030236392A1
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Pred. No. 4.6e-26;
0; Mismatches 11
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                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: chemically treated genomic DNA US-10-311-455-1064
                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 1064
LENGTH: 16724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1064, Application US/10311455 Publication No. US20030143606A1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION
                                                                                                                                                                                                              Query Match 5.2%;
Best Local Similarity 46.2%;
Matches 141; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
TITLE OF INVENTION: cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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NAME/KEY: unsure
LOCATION: (3294164)
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                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
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                                                                                         AAGTTGAGATGGTGTTATTTTAGTTTTGGGTTATAGAGTGAGATTTTATTTTAAAA 13754
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CAGATGGATTTTAAAAAGTGTTAGATCTTTCCAATGAACACTAATAGAGTACTCTGCTCT
                              TTAATCCTGATAAAGAAGATTGTTGGGAAGCTCTTTGAAAAAAATTTTAAATTGTGGCA 305
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50.7%;
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Pred. No. 12;
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Pred. No. 0.85;
0; Mismatches
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US-10-240-485-90
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TITLE OF INVENTION: Diagnosis of Diseases Associated with
TITLE OF INVENTION: Metastasis
FILE REFERENCE: 5013.1007
CURRENT APPLICATION NUMBER: US/10/240,485
CURRENT FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: PCT/EP01/03970
PRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , OTHER INFORMATION: chemically treated genomic DNA US-10-240-485-90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 90, Application US/10240485 Publication No. US20030148327A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 202
SEQ ID NO 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 141; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: PIEPENBROCK, Christian APPLICANT: BERLIN, Kurt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13995 AAAAA 13999
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GATAA 430
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                                                                                            TGGCTGGATTTTTCAGAGAATGGCAATGGTCTCTGCGATGTCCTGGGTCCTGTATTTGTG 425
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Pred. No. 0.85;
0; Mismatches 164;
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GENERAL INFORMATION:

APPLICANT: Brandt, Kevin S.

APPLICANT: Gaines, Patrick J.

APPLICANT: Stinchcomb, Dan T.

APPLICANT: Stinchcomb, Dan T.

APPLICANT: Wisnewski, Nancy

ITITE OF INVENTION: NUCLEIC ACID MOLECULES, PROTEINS AND USES THEREOF

FILE REFERENCE: FC-6-C1

CURRENT APPLICATION NUMBER: US/09/991,936

CURRENT FILING DATE: 2001-11-21

FRIOR APPLICATION NUMBER: US/09/543,668

PRIOR APPLICATION NUMBER: US/09/543,668

PRIOR APPLICATION NUMBER: 05/128,704

PRIOR APPLICATION NUMBER: 05/128,704

PRIOR APPLICATION NUMBER: 05/128,704

PRIOR APPLICATION NUMBER: 05/128,704

PRIOR TILING DATE: 1999-04-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-311-455-2108
Sequence 2108, Application US/10311455; Publication No. US20030143606A1; GENERAL INFORMATION:
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IS-09-991-936-1045/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 5.2%;
Best Local Similarity 47.9%;
Matches 105; Conservative
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                                                                                                                    SEQ ID NO 2108
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ORGANISM: Ctenocephalides felis
-09-991-936-1045
                                                                                                                                                                     APPLICANT: OLEK, Alexander
APPLICANT: PIEPEMBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
TITLE OF INVENTION: Cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
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                                                                                                                                                      NUMBER OF SEQ ID NOS: 2424
                                              ORGANISM: Artificial Sequence
                                                                                TYPE: DNA
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INFORMATION: chemically treated
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Pred. No. 0.16;
0; Mismatches 114;
genomic
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  DNA
(Homo sapiens)
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GENERAL INFORMATION:

APPLICANT: OLEK, Alexander
APPLICANT: BIEDEMBROCK, Christian
APPLICANT: BERLIN, Kurt
ITTLE OF INVENTION: Diagnosis of Diseases Associated with the
ITTLE OF INVENTION: Diagnosis of Diseases Associated with the
ITTLE OF INVENTION: Ottosine methylation
FILE REFERENCE: 5013.1014

CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: COT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 2046
LENGTH: 40862
TYPE: DNA
OPERANTSM. Artificial Sequence
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US-10-311-455-2046
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                                                                                                                                                                                                                                                               Query Match
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AATTGAAATAG 154
                                                                      TTTTAAGTAAAATATTGGAGAAGA
                                                                                                            TGATAAAGAAGATTGTTGGGAAGCTCTTTGAAAAAAATTTTAAATTGTGGCACAGATGG 312
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Pred. No. 1.
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RESULT 10 US-10-311-455-78

Sequence 78, Application US/10311455 Publication No. US20030143606A1 GENERAL INFORMATION:

US-10-257-166-2

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CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: ECT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR REPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR REPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 78
LENGTH: 17869
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                                                                                                                                       SEQ ID NO 2
LENGTH: 17869
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TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
TITLE OF INVENTION: cytosine methylation
FILE REFERENCE: 5013.1014
                                                                                                                                                                             NUMBER OF SEQ ID NOS: 178
                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: PCT/EP01/07470 DE 10032529.7
                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/257,166
CURRENT FILING DATE: 2002-10-07
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Method and Nucleic Acids for Analysing the Methylation
TITLE OF INVENTION: Genes Implicated in Pharmacogenomics
FILE REFERENCE: 5013.1011
                                                                                                                                                                                                                                            PRIOR FILING DATE: 2001-06-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: unsure
LOCATION: 3465, 3586
OTHER INFORMATION: n is a or g
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                                                      FEATURE:
OTHER INFORMATION:
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                                                                                              ORGANISM: Artificial Sequence
                                                                                                                          TYPE: DNA
NAME/KEY: unsure LOCATION: (3465,
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                                                           chemically treated
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APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Ass
TITLE OF INVENTION: cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DC 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DC 1043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEG ID NOS: 2424
SEQ ID NO 253
LENGTH: 13511
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US-10-311-455-253
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Best Local S
Matches 83
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                                                                                                                                                                                                                                                                                         Best Local Similarity Matches 98; Conser
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ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: unsure LOCATION: 4623
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Local Similarity 54.2%;
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AATGATGAATTTTA 12217
                                  AATGAACACTAATA 351
                                                                                                       CTTTGAAAAAATTTTAAATTGTGGCACAGATGGATTTTAAAAAGTGTTAGATCTTTCC 337
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Publication No. US20030143606A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/10312841 Publication No. US20030186277A1 GENERAL INFORMATION:
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LENGTH: 9268
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APPLICANT: PIEPENBROCK, Christian
APPLICANT: BETLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
TITLE OF INVENTION: Cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: PCT/EPO1/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER: DE 5000-09-01
PRIOR FILING DATE: 2000-09-01
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                                                                                                                                                                       NUMBER OF SEQ ID NOS:
SEQ ID NO 2
                                                                                                                                                                                           APPLICANT: Epigenomics AG
TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des
FILE REFERENCE: E01/1208/WO
CURRENT APPLICATION NUMBER: US/10/312,841
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 2
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ORGANISM: Artificial Sequence
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FEATURE:
NAME/KEY: unsure
LOCATION: (379615)
                                                                  OTHER INFORMATION: chemically treated genomic DNA
                                                                                 FEATURE:
                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                TYPE: DNA
                                                                                                                                                   ENGTH: 3673778
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Local Similarity 47.8%;
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Search completed: April Job time : 373 secs

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Matches 117; Conserv
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SEQ ID NO 1248
LENGTH: 13038
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                                                                                                                                                                              Matches
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CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: OLEK, Alexander APPLICANT: PIEPENBROCK, Christian APPLICANT: BERLIN, Kurt
                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
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Pred. No. 4.7;
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Maximum DB seq length: 2000000000
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Copyright (c) 1993 - 2004 Compugen Ltd.
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BC025746
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1934)
                                                                                                                                                                                                              Direct Submission
Submitted (06-MAR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
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AK049880
BU275101
BU272791
AW955725
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AY404312
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CB730363
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H23443 Ym5299 r1

BB653506 BB653506

AK049880 Mus muscu

BU275101 603532890

BU275101 603532890

BU275101 603532890

BU275101 603532890

AW955725 EST367795

R67171 Yh08d07.r2

R56299 yg90b04.r1

T81284 yd06902.r1

T81284 yd06902.r1

T81284 yd06902.r1

T81287 AG06902.r1

T81287 AG06902.r1

T81287 AG06902.r1

T81288 yd06902.r1

T81288 yd06902.r1

T81288 yd06902.r1

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T81288 yd06902.r1

T81288 yd06902.r1

AA365792 EST76613

T80333 yd07d07.r1

AA4641769 cm11b05.w

BB653101 BH653101

AL861103 AL861103

AL861104 AL861104

BY283942 BY283942

BY283942 BY283942

BY283942 BY283942

BY283473 BY283473

BW049600 UT-M-BH1

BY283473 BY283473

BW101385 BX101385

R13004 yf71b07 r1

AQ318831 RPCT11-10

BY283033 BY250323

BY210325 BX101385

CG561170 OST182559

AY404310 Homo sapi

AY404310 Homo sapi
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BF652347 275877 MA
BU615139 UI-M-FR0-
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AK050001 Mus muscu
CK001752 AGENCOURT
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HTC 04-MAR-2003

Mus muscu

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FEATURES
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Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Laric,P., Legaspi,R.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNI at: http://image.llnl.gov Series: IRAK Plate: 49 Row: b Column: 3
This clone has the following problem: retained intron.
Location/Qualifiers
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AAAGTGGCTGGAACAAGAAGAAACCGGCCTTCTTGCGTCGATGCCTCCATAGTGATTGGG
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/tissue_type="Brain, adult,
/clone_lib="NIH_MGC_114"
/lab_host="DH10B"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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SOURCE
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                                                             AGGTGAAAATGACAAGGTTTCCACCCCTCAAACCTTGGCTCCTTTTCTGACAATACAGTC
                                 AGGTGAAAATGACAAGGTTTCCACCCCTCAAACCTTGGCTCCTTTTCTGACAATACAGTC
                                                                                                                                                                                                                                                                             98.5%;
nilarity 99.6%;
Conservative :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/clone="CSODF003YG18"
/tisste_type="fetal"
/dev_stage="fetal"
                                                                                                                                                                                                                                                                                                                                                                                   /clone lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-Oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and ECORV sites of the pCMVSPORT 6
vector. Library was not normalized."
                                                                                                                                                                                                                                                                             Score 800.2; DB pred. No. 1e-218; 2; Mismatches
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AAATGGTGGTGTGAGATGGAGCCTTGCCTAGAAGGAGGAGAAGAATGTAAGACACTCCCTGAC
                                             AATTCTGGATGGATGTGCGCAACAGGCAACAAATTAAGACCACGAGAATTCACCCAAGA 780
                                                                                                                                           AAATGGTGGTGAGATGGAGCCTTGCCTAGAAGGAGAAGAATGTAAGACACTCCCTGAC 728
<u>ARTTCTGGATGGATGTGCGCAACAGGCAACAAAATTAAGACCACGAGAATTCACCCAAGA</u>
               788
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AL534074 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone CSODF003YG18 5-PRIME, mRNA sequence.
AL534074 AL534074 AL534074 AL534074 AL534074 AL534074.2 GI:30539521 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 929)

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2511.f

Contact: .Feng Liang Email: fliang@lifetech.com URL:

http://fulllength.invitrogen.com/ InVitrogen Corporation 1600

Faraday Avenue Genoscope sequence ID: CSODF003BD09QP1.

Location/Qualifiers gi:12797567.

61 TTATCTCCCCATCACTTCAAAGGTCTCGTCAGGCAGAGGTGACGCCAGGAGATGATTTAA 120 CACTGGAGTGGGGATGGTCCATCGGCAACTATAAACTGATTCTCATCAGGAAACTGCACA 125 TTATCTCCCCATCACTTCAAAGGTCTCGTCAGGCAGAGGTGACGCCAGGAGATGATTTAA Indels Length 929; ۳. Gaps

185

245 180 60

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TITLE
JOURNAL
COMMENT
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SOURCE
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                        FEATURES
                                                                                                                                                                        AUTHORS
                              Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 2511.f,

Contact: Feng Liang Email: fliang@lifetech.com URL:

http://fulllength.invitrogen.com/ InVitroGen Corporation 1600

Faraday Avenue Genoscope sequence ID: CS0DF015DF12QP1.
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EX460561 GI:31035Z11
                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 940)
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                    Location/Qualifiers
organism="Homo sapiens"
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/mol type="mRNA"
/db xref="taxon:9606"
/clone="CSODF015YL24"
/tissue_type="FETAL BRAIN"
/dev_stage="fetal"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pcMVSPORT_6; lst strand cDN7
/notes primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT_6
vector. Library was not normalized."
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GTGAAAATGACAAGGTTTCCACCCCTCAAACCTTGGCTCCTTTTCTGACAATACAGTCTG ATCTCCCCATCACTTCAAAGGTCTCGTCAGGCAGAGGTGACGCCAGGAGATGATTTAAAG CTGGAGTGGGGATGGTCCATCGGCAACTATAAACTGATTCTCATCAGGAAACTGCACATT GAAAAGTGGCTGGAACAACAAGAAACCGGCCTTCTTGCGTCGATGCCTCCATAGTGATTG GTTGTAACAAGAATCGCATTGAGGAGCGGTCACAAACAGTAAAGTGTTCCTGTCTACCTG AGCAGCATCACCTGCACAGACCAGAAGGAGGACGTGTGAAGTGATAGCAGCACACCGAT ATTIGTGGATAAGIGCTTGIGCAAIGCTACICTGCCAIGGAICCCTTCAGCACACITTICC CTGCTCTTGGCTGGATTTTTCAGAGAATGGCAATGGTCTCTGCGATGTCCTGGGTCCTGT TGTGGCACAGATGGATTTTAAAAAGTGTTAGAGTCTTTCCAATGAACACTAATAGAGTACT TITITITAATCCTGATAAAGATAGATTGTTGGGAAGCTCTTTGAAAAAAATTTTAAAT TTTTTTTAATCCTGATAAAGA-AGATTGTTGGGAAGCTCTTTGAAAAAAAATTTTAAAT AATGRACCCGATGTCTTTTTTTTTTACTGTGGAAATAGGATCGGAAGAGAGTAACATTTTT GTGAAAATGACAAGGTTTCCACCCCTCAAACCTTGGCTCCTTTTCTGACAATABAGTCTG ATCTCCCCATCACTTCAAAGGTCTCGTCAGGCAGAGGTGACGCCAGGAGATGATTTAAAG CCGGAATTCCCGGGATCCATCGGCAACTATAAACTGATTCTCATCMSGAAACTGCACATT ACAATTCTGGATGGATGTGCGCAACAGGCAACAAATTTAAGACCACGAGAATTCACCCAA CTGCTCTTGGCTGGATTTTTCAGAGAATGGCAATGGTCTCTGCGATGTCCTGGGTCCTGT GAACCTAACAGAAGCATTTGTGGTAGTAAAGGAA GAAAAGTGGCTGGAACAACAAGAAACCGGCCTTCTTGCGTCGATGCCTCCATAGTGATTG TGTGGCACAGATGGATTTTAAAAAGTGTTAGATCTTTCCAATGAACACTAATAGAGTACT Conservative rggtgtgagatggagccttgcctagaaggaagaatgtaagacactccctg 94.5%; 10; Score 767.2; DB 13 Pred. No. 3.1e-209; 0; Mismatches 9; DB 13; Length 940; 4. 358 298 182 122 109 62 829 598 589 538 529 478 469 418 409 349 289 239 229 **169** 658 649 769 718

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REFERENCE
AUTHORS
TITLE
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B1756155
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collections (1999)
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Plate: LLAM11501 row: f column: 15
High quality sequence stop: 793.
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                                                                                                                                                                                   AAGGTGAAAATGACAAGGTTTCCACCCCTCAAACCTTGGCTCCTTTTCTGACAATACAGT
                                                                                                                                                                                                                         ATTATCTCCCCATCACTTCAAAGGTCTCGTCAGGCAGAGGTGACGCCAGGAGATGATTTA
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TGTGGCACAGATGGAITTTAAAAAGTGTTAGATCTITCCAATGAACACTAATAGAGTACT 358
                                                              TTTTTTTAATCCTGATAAAGAAGATTGTTGGGAAGCTCTTTGAAA-AAAAATTTTAAAT 298
                                                                                                      AAGGTGAAAATGACAAGGTTTCCAACCCCTCAAACCTTGGCTCCTTTTCTGACAATACAGT
                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            /clone lib="NIH_MGC 114"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1;
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: EcoRV (destroyed); RNA source anonymous pool of 6
male-brains, age range 23-27 yo. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.5 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 019. Note:
this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5200142"
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mol_type="mRNA"
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98.2%;
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sapiens cDNA clone IMAGE:5200142 5',
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1.9e-180;
hes 5;
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603021235F1 NIH_MGC_114 Homo sapiens
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://image.llnl.gov
Plate: LLAMI1479 row: f column:
High quality sequence stop: 680.
Location/Qualifiers
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          found through the I.M.A.G.E. Consortium/LLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution information can Clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGTGGCACAGATGGATTTTAAAAAAGTGTTAGATCTTTCCAATGAACACTAATAGAGTACT
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clome="IMARGE:5191688"
/lab_host="DH10B"
/clome lib="NIH MGC 114"
/clome lib="NIH MGC 114"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: l
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1
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RESULT 6
AK050001
                                                                    ACCESSION
VERSION
                  SOURCE · ORGANISM
                                                     KEYWORDS
                                                                                                                                                DEFINITION
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                                                                                                                       AK050001 3258 bp mRNA linear HTC 20-SEP-
Mus musculus adult male hippocampus cDNA, RIKEN full-length
enriched library, clone:C630045F22 product:unclassifiable, full
               HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
                                                                  AK050001
AK050001.1 GI:26093743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                             GAAAAGTGGCTGGAA--CAACAAGAAACCGGCCTTCTTGCGTCGATGCCTCCATAGTGAT 656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CACTGGAGTGGGGATGGTCCATCGGCAACTATAAACTGATTCTCATCAGGAAACTGCACA
                                                                                                                                                                                                                                                                                              TGGGAA-ATGGTGGTGTG-AGATGGAGCCTTGCCTAGAAGG 695
                                                                                                                                                                                                                                                                                                                                                                                                         TTGTAACAAGAATCGCATTGAGGAGCGGTCACCAAACAGTAAAGTGTCCCTGTCTACCTG
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                                                                                                          sequence.
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97.6%;
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Pred. No. 4.4e-164;
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Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishi, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, S., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y., RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer denome Res. 10 (11), 1757-1771 (2000)
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1. Nature 420, 563-573 (2002)

2. 6 (bases 1 to 3258)

2. 8 (bases 1 to 3258)

2. 8 Adachi J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Adachi J., Aizawa, K., Akimura, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hiramoto, K., Hiraoka, T., Hirozane, T., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Katoh, H., Kowai, J., Kojima, Y., Koh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kouda, M., Katoh, H., Kowai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Muratta, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku, Akahira, S., Takada, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (16-UII-2001) Yoshihide Hayashizaki, The Institute of Submitted (16-UII-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URLihttp://genome.gssc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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Analysis of the mouse transcriptome based of 60,770 full-length cDNAs
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
                                                                                                                                                                                                       Encyclopedia Project of Genome Exploration Research Group
Genomic Sciences Center and Genome Science Laboratory in F
Division of Experimental Animal Research in Riken contribu
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/clone Tib="RIKEN full-length enriched mouse cDNA library"
/dev stage="adult"
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/db_xref="MGI:2417712"
/db_xref="MGI:2417712"
/db_xref="reaxon:10090"
/clone="C630045F22"
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National Institutes of Health, Mammalian Gene Col
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: Professor Miklss Palkovits
cDNA Library Preparation: Michael Brownstein / T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: NDCM260 row: j column: 01 High quality sequence stop: 579.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1. (bases 1 to 672)
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                                                                                    TGGAAATAGGATCGGAAGAGAGTAACATTTTTTTTTAATCCTGATAAAGAAGATTGTTG 270
                                                                                                                                                                  AGGCAGAGGTGACGCCAGGAGATGATTTAAAGGTGAAAATGACAAGGTTTCCACCCCTCA 150
     GGAAGCTCTTTGAAAAAAATTTTAAATTGTGGCACAGATGGATTTTAAAAAGTGTTAGA 330
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//clone_lib="NIH_MGC_227"
//note="Organ: brain/CNS; Vector: pDNR-LIB; Site_1: Sfil
//note="Organ: brain/CNS; Vector: pDNR-LIB; Site_1: Sfil
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/mol type="mRNA"
/db_xref="taxon:9606"
/clone="INAGE:30718008"
/tissue_type="Bulk tissue_f
/lab_host="DH10B_TonA"
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BU118807.1
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1 (bases 1 to 768)

1 (bases 1 to 778)

1 (bases 1 to 788)

2 (bases 1 to 788)

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12445392
Contact: Simon Hubbard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Department of Biomolecular Sciences University of Manchester Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Simon. Hubbard@umist.ac.uk.
                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/strain="Compton Line 1
/db_xref="taxon:9031"
/clone="ChEST137f15"
/note=Torgan: brain; Vector: pBluescript II KS(+); Site_1: EcoRI, Site_2: Not1; Modification of pBluescript II KS(+) [Stratagene] vector to accommodate cDNA produced with the T-trimmed protocol (Construction of uni-directionally cloned cDNA libraries from messenger RNA for improved 3' end DNA sequencing by Glenn Fu, et al. U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI. Ligate in double stranded adaptor containing BsgI and BamHI sites [5'ggccgcgtgcagccccggatccgaaaaaaaa]
                                                                                                                                                                                                                             /dev_stage="adult/
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                               tissue_type="not cerebrum
                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Gallus gallus"
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BF652347.1
EST.
    Smith, T.P.L., Grosse, W.M., Freking, B.A., I Casas, E., Wray, J.E., White, J., Cho, J., Fal Bennett, G.L., Heaton, M.P., Laggreid, W.W., Chitko-McKown, C.G., Pertea, G., Holt, I., K.
                                                                                                Bovidae; Bovinae; Bos.
1 (bases 1 to 506)
                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                         Bos taurus (cow)
                                                                                                                                                                                                                                                                                                            BF652347
275877 MARC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAAGACCACCAGAATCCACCCAAGGACCTAACAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTCTGCGATGTCCTGGGTCCTGTATTTGTGGATAAGTGCTTGTGCAATGCTACTCTGCCA 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTATT----AAAAATCCCTTATTGTGGTGCAGATGGATTTTAAAAAGTGTTAGACCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTGTAACAAGAGATTTTTTTTTTGTCCTCGTAATCCTGATAAAGAAGATTATTGGGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAAGACCACGAGAATTCACCCAAGAACCTAACAGA 790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGTTGATGCTTCAATAGTGATTGGGAAATGGTGGTGAGATGGAGCCCTGCCTAGAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGTAAAATGCTCCTGTCTACCTGGGAAAGTGGCTGGGACTACACGAAACAGACCTTCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGTAAAGTGTTCCTGTCTACCTGGAAAAGTGGCTGGAACAACAAGAAACCGGCCTTCTTG 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGAAGTTATAGCAGCACACAGATGCTGTAATAAGAATCGAATTGAGGAAAGATCACAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGAAGTGATAGCAGCACACCGATGTTGTAACAAGAATCGCATTGAGGAGCGGTCACAAAC 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCTGCAATGTCCTGGGTCCTGTATTTGTGGATAAGTGCCTGTGCAATGCTGCTCTGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCAATGAACACTAATAGAGTGCTCTGCTCTTGGCTGGATTACTCAGAGAATGGCAGTGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCTTTGAAAAAAATTTTAAATTGTGGCACAGATGGATTTTAAAAAGTGTTAGATCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Pred. No. 2.4e-125;
0; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                    506
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                                                  Fahrenkrug, S
                                                Roberts, A.J., s
         Karamycheva,S.,
                                                                                                                                                                                                                                                                                                            sequence
                            Rohrer,
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                                                                               Stone, R.T.,
       Liang, F.
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MEDLINE
PUBMED
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                                                                                                                                                    689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 65 row: M column: 8
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence evaluation of four pooled-tissue normalized bovine libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Single pass sequencing. Bases call
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quackenbush,J. and Keele,J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCR PRimers
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                                                                                                                                                                                                                                                                                                        AAACCGCATTGAGGAGCGGTCGCAAACAGTCAAGTGTTCCTGTCTACCTGGGAAAGTGGC
                                                                                                                                                                                                                                                                                                                                                    GAATCGCATTGAGGAGCGGTCACAAACAGTAAAGTGTTCCTGTCTACCTGGAAAAGTGGC 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCTGCACAGACCAGAAGGAGGGACGTGTGAAGTGATAGCAGCACACCGATGTTGTAACAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGGATTTTTCAGAGAATGGCAATGGTCTCTGCGATGTCCTGGGTCCTGTATTTGTGGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATCCTGATAAAGAAGA-TATTGGGAAGCTCTTTTTAAAAAAATCTTCAATTGTGGCACAG
                                              ATGGATGTGCGCAACAGGCAACAAAT 755
                                                                                                                                                 GTGTGAGATGGAGCCTTGCCTAGAAGGAGAAGAATGTAAGACACTCCCTGACAATTCTGG 728
                                                                                                                                                                                                                                                    TGGAACAACAAGAAACCGGCCTTCTTGCGTCGATGCCTCCATAGTGATTGGGAAAATGGTG
                                                                                                                                                                                                                                                                                                                                                                                                        CCTGCACCGACCAGAAGGAGGGACGTGTGAAGTGATTGCTGCGCACAGATGTTGTAATAA
                                                                                                                                                                                                     TGGAACAACAAGAAACCGACCTTCCTGTGTCGATGCCTCCATTGTGATCGGGAAATGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pCMV SPORT6; Site 1: Not1; Site 2: Sal1; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and fetal longissimus muscle."
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mol_type="mRNA"
db_xref="taxon:9913"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lib="MARC 3BOV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 442.2; DB 10;
Pred. No. 7.7e-116;
D; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     called and alt trimmed with phred by cross_match with the -minscore
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COMMENT
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                   Matches 575;
                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                           Local Similarity
64
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                                                                                                                                                                                                                               23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@wilowa.edu
This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Muri 1 (bases 1 to 706)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BU615139 706 bp mRNA linear EST 20-FEB-
UI-M-FR0-cbe-1-08-0-UI.r1 NIH BMAP FRO Mus musculus cDNA clone
UI-M-FR0-cbe-1-08-0-UI 5', mRNA sequence.
BU615139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: pYX-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The following repetitive elements were found in this cDNA sequence: 218.261, >(GAAAA)n#Simple_repeat (matched compli
                                                                                                                                                                                                                CGGCAACTATAAACTGATTCTCATCAGGAAACTGCACATTATCTCCCCCATCACTTCAAAG
                                                                                                                            GTCTCGTCAGGCAGAGGTGACGCCAGGAGATGATTTAAAGGTGAAAATGACAAGGTTTCC 142
                                                                                                                                                                                CGTNGGCTATAAACTGCTTCTCATCAGGAAACT--ACATTAGCTCACCATCACTTCAAAG
                                                                                                                                                                                                                                                                                                                                                                                              /tissue type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab host="PH108 (T1 phage resistant)"
/clome lib="wnH108 (T1 phage resistant)"
/clome lib="wnH108 (T1 phage resistant)"
/note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Sonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
grimer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector: The library tag
sequence located between the Not I site and the polyA tail
is AGCGAGACAG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."
                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/strain="C57BL/6"
/db_xrefe"taxon:10090"
/clone="UI-M-FR0-cbe-1-08-0-UI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Socation/Qualifiers
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                                                                                                                                                                                                                                                                                                     54.3%;
81.2%;
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                                                                                                                                                                                                                                                                                                        Score 440.8; DB 13
Pred. No. 2.1e-115;
                                                                                                                                                                                                                                                                                   Mismatches
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REFERENCE
AUTHORS
TITLE
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VERSION
KEYWORDS
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1 (bases 1 to 975)

11,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On Feb 13, 2001 this sequence version replaced gi:12797458.

Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL533965 Homo sapiens FETAL BRAIN Homo sapiens CSODF003YN23 5-PRIME, mRNA sequence.
                                                                                                                     Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2511.f
Contact: Feng Liang Email: filang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroden Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODF003CG12QP1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL533965
AL533965.2 GI:30539311
                                                                                                                                                                                                                                          Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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/clone="CS0DF003YN23"
/tissue_type="FETAL BRAIN"
/dev_stage="fetal"
                                                                      /organism="Homo sapiens"
/mol_type="mRNA"
                                                        /db_xref="taxon:9606"
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Best Local Similarity
Matches 436; Conserv
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                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 468)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Parsonskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                            H23443
ym52g09.rl Soares infant brain 1NIB Homo sapiens cDNA clone
                                                                                         Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. J
                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                 H23443.1 GI:892138
                                                                                                                                                                                                                                                                                                                                                                              H23443
                                                                                                                                                                                                                                                                                                                                                                                            ÎMAGE:51993 5',
                                                                                                                          Contact: Wilson RK
                                                                                                                                             Unpublished (1995)
                        Email: est@watson.wustl
Insert Size: 948
                                                                                                                                                           The WashU-Merck EST Project
                                                                                                                                                                          Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGAACCTAACAGAAGCATTTGTGGTAGTAAAGGAA
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314 286 1810
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95.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                 sequence.
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Pred. No. 1.2e-113;
9; Mismatches 11;
            360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   966
                                                                                              Louis,
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ð

EST 06-JUL-1995

/clone\_lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNI
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

TGACAATTTCTGGATGGATGTGCGCAACAGGCAACAAAATTAAGACCACGAGAAATTCACCC TGGGAAATGGKGGKGTGAGATGGAGCCTTKCCTAKAAGGAGAAGAATGTAAGACACTCCC TGGGAAATGGTGGTGTGAGATGGAGCCTTGCCTAGAAGGAGAAGAATGTAAGACACTCCC TGGAAAAGTGGCTGGAACAACAAGAAACCGGCCTTCTTKCGTCGATGCCTCCATAGTGAT TGGAAAAGTGGCTGGAACAACAAGAAACCGGCCTTCTTGCGTCGATGCCTCCATAGTGAT ATGTTGTAACAAGAATCGCATTKAGGAGCGGKCACAAACAGTAAAGTGTTCCTGTCTACC ATGTTGTAACAAGAATCGCATTGAGGAGCGGTCACAAACAGTAAAGTGTTCCTGTCTACC CCAGCAGCATCACCTGCACAGACCAGAAGGAGGACGTGTGAAGTGATAGCAGCACACCG CCAGCAGCATCACCTGCACAGACCAGAAGGAGGGACGTGTGAAGTGATAGCAGCACCACCG GTATTTGTGGATAAGTGCTTGTGCAATGCTACTCTGCCATGGATCCCTTCAGCACACTTT GTATTTGTGGATAAGTGCTTGTGCAATGCTACTCTGCCATGGATCCCTTCAGCACACTTT CTTTCCTGTCGAATGTTCTCTTTAGAGAATGGCAATGTCTCTGCGATGTCCTGGGTCCT CTCTGCTCTTGGCTGGATTTTTCAGAGAATGGCAATGGTCTCTGCGATGTCCTGGGTCCT Length 975; 0 476 530 776 656 596 536 470 416 716 650 590 830 710

(bases 1 to 692)

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RESULT 13
BB653506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ш
                                                                                                                                            BB653506 RIKEN full-length enriched, adult male h musculus cDNA clone C630045F22 5', mRNA sequence.
BB653506
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                  Mus musculus
                                                                                                                          BB653506.1 GI:16487345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTGAAGTGATAGCAGCACACCGATGTTGTAACAAGAATCGCATTGAGGAGCGGTCACAAA 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGGATCCCTTCAGCACACTTTCCAGCAGCAGCATCACCTGCACAGACCAGAAGGAGGAGGGACGT 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTCTGCGATGTCCTGGGTCCTGTATTTGTGGATAAGTGCTTGTGCAATGCTACTCTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCGTCGATGCCTCCATAGTGATTGGGAAATGGTGGTGTGAGATGGAGCCTTGCCTAGAAG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAGTAAAGTGTTCCTGTCTACCTGGAAAAAGTGGCTGGAACAAGAAGAAAACCGGCCTTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAGTAAAGTGTTCCTGTCTACCTGGAAAAGTGGCTGGAACAACAAGAAACCGGCCTTCTT 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GIGAAGIGATAGCAGCACACCGAIGTIGTAACAAGAATCGCATTGAGGAGCGGTCACAAA 180
                                                                                                                                                                                                                                                                                                                                                TTAAGACCACGAGAATTCACCCAAGAACCTAACAGAAGGCTTTGTTGTAGTAAAGGGA 418
                                                                                                                                                                                                                                                                                                                                                                                                                                               quality sequence stop: 360.
                                                                      musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Homo sapiens"
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Pred. No. 2.7e-106;
0; Mismatches 6;
                                                                                                                                                                                                 mRNA linear EST 26-(
d, adult male hippocampus
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AUTHORS
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                                                         ORIGIN
       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
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Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,
Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
Ohno,M., Okazaki,Y., Okido,T., Salto,R., Sakai,C., Sakai,K.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Sushiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e mouse tissues
                                                                                                                                                                                                   prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGAGTTAATTAATTAATTCCCCCCCCCCC 3']"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="hippocampus"
/dev_stage="adult"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone="C630045F22"
                                                                                                                                                                                                                                                                                                                                                                                                                              _lib="RIKEN full-length enriched, adult male
               Score 389.2;
                 멂
                 10;
               Length 692
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RESULT 14
AK049880
                                                                                                                                                 REFERENCE
AUTHORS
                                                                                                                                                                                                                                                    SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                          ACCESSION
VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                 AK049880 2412 bp mENA linear HTC 20-
Mus musculus adult male hippocampus cDNA, RIKEN full-length
enriched library, clone:C630007B19 product:unclassifiable,
                                                                                             Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA
Meth. Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                                                                            Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                   AK049880.1 GI:26093679
HTC; CAP trapper.
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Carninci, P.,
                                                                                                                                                                                                                                                                                                                                                                              insert sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCT 686
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Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
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Rodentia;
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0; Mismatches 99;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc:riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Nyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N. Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takada, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group
Genomic Sciences Center and Genome Science Laboratory in R
Division of Experimental Animal Research in Riken contribu
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6 (bases 1 to 2412)
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Analysis of the mouse transcriptome of 60,770 full-length CDNAs
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                                                                                                                                                                                                                                                                                                                                  prepare mouse tissues.
Please visit our web site for further details.
     /tissue_type="hippocampus"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
1...7412
                                                                                                                               /db_xref="taxon:10090"
/clone="C630007B19"
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                                                                                                                                                                                                                                                    Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute
                                                                                                                                                  PO Box 88, Manchester,
Tel: 01612008930
Fax: 01612360409
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                                                                                               Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
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                       /organism="Gallus gallus"
/mol_type="mRNA"
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/strain="Compton Line 15I"
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AATGGTGGTGT-GAGATGGAGCCTTGCCTAGAAGGAGAAGGAGTGTAAGA-CACTCCCTGA
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/note="Organ: brain; Vector: pBluescript II KS(+); Site_1:
/note="Organ: brain; Vector: pBluescript II KS(+); Site_1:
/note="Organ: brain; Vector: pBluescript II KS(+); Site_1:
/note="Organ: brain; Vector: pBluescript was
constructed from 1 million independent clones: cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
/note for the first strand synthesis reaction.
/note following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
ECORI, size-selected, and cloned into the NotI and ECORI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 928-9232 and Bonaldo et al., Ganome Research 6
(1996: 791, except that a significantly longer
reannealing hybridization was used."
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lab_host="DH10B"
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Search completed: April 9, 2004, 15:45:13 Job time : 2566 secs	794 TAAATCTGGATGG 806	720 CAATTCTGGATGG 732	734 AATGGTGGTGTGGAAATGGAGCCTGCCTAGAAGGGAGAGGAATGTACGACCGTTGCCTGA 793